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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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E40093
E40091
E40090
E40089
AR076817
E15125
AR076816
               AR146852
ES5065
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BD188672
BD188674
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AR146856
AR146857
E55069
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E40093 Plant promo
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AR076817 Sequence
E15125 Promoter: 7
AR076816 Sequence
E15124 Promoter: 7
AR14682 Sequence
E55065 Plant promo
D188672 Promotor
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ED188674 Promotor
AR146855 Carrot gCHS
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E55069 Plant promo
E55069 Plant promo
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CR847802 Danio rer	AC104073 Homo sapi	AC104069 Homo sapi	AL034556 Plasmodiu	CR392006 Danio rer	AC126283 Homo sapi	L36897 Saccharomyc	AX599046 Sequence	AX598900 Sequence	CR356223 Danio rer	AL035476 Plasmodiu	CR388025 Danio rer	AX344555 Seguence	AC091214 Homo sapi	AL929352 Plasmodiu	AL928596 Human DNA	U37541 Drosophila	U11584 Drosophila	AL031746 Plasmodiu	AE001398 Plasmodiu	AC105425 Homo sapi	AX599046 Sequence	CR382399 Plasmodiu	AE014832 Plasmodiu	AC093899 Homo sapi	AE014839 Plasmodiu

## ALIGNMENTS

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                                                             Query Match
Best Local Similarity
Matches 2052; Conserv
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TITLE
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PN JP 2000166577-A/1

PN JP 2000166577-A/1

PD 20-UTN-2000

PF 01-OCT-1999 JP 1999281475

PR SATOMI NISHIKAWA, KENJI OEBA

PI SATOMI NISHIKAWA, KENJI OEBA

PC C12N15/09, A01H5/00, C12N1/21, C12N5/10// (C12N5/10, C12R1:91), PC

C12N15/00, C12N5/00, C12R1:91)

CC C12N5/00, (C12N5/00, C12R1:91)

CC FH Key Location/Qualifiers

FT promoter (1) . (2052).
                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 2052)
Nishikawa, S. and Oeda, K.
Plant promoter and terminator
Patent: JP 200016577-A 1 20-JUN-2000;
SUMITOMO CHEM CO LTD
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JP 2000166577-A/1.
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Plant_promoter and terminator.
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                  CATGTGTGCCCTACAGCACATAGGGCCTGTTTGGTTGAGAGAAGCAGAAGCTGCTTCTGA 60
CATGTGTGCCCTACAGCACATAGGGCCTGTTTGGTTGAGAGAAGCAGAAGCTGCTTCTGA
                                                             100.0%; ilarity 100.0%; Conservative 0,
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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1021 TGATCATCCATTAAAACCTTGTTAAAACAAATTCAATGAGATAAAATATCTTACAATGAA 1080	TTAAACGAAAATCATTTTATAACATGTCTCTCGGCTGTCATTATAATAGGGATCACTTAC 10	1 1		81				41	•		1961	01		TCTCATTTCTACTCCACTTCTTTGCTATAAGCAAGAAATCACTTCTTTTAAGCTAACCCA	121 TACTAACTTCTCTCACAACTTCCGCTTCTTTTCCAAACACTTTATTAACTTTTTACT 180 121 TACTAACTTCTCTCACAACTTCCGCTTCTTTTCCAAACACTTTATTAACTTTTTACT 180 121 TACTAACTTCTCTCACAACTTCCGCCTTCTTTTCCAAACACTTTATTAACTTTTTACT 180	61 CTTCTTCTTTTGACCTGTTTGTATAAAGAAGTAGAAATATTTTAAAAAGCTGCGAA 120 
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RESULT 2 E40093 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	ОУ	Db Qy	B 8	용 성	8 8	Db Qy	B &	A 4	D Qy	р Q	Db Qy	Qγ	dg VQ	B 8	B & :	Db
E40093  Plant promoter and terminator.  P40093.1 GI:18627209  JP 2000166577-A/7.  unidentified  M unidentified		1981 CACATCAATCTTACACCACAAACCTTGAGCTTAATTTTTCTACTTATTCTCAGCAATAAC 2040 	1921 AACACCTCAACATTGATGTTAGCGTACTATAAATAGGTGCTCTTGGTGCTCTACTATCAT 1980 	1861 GATTGGAATCCTTTTCTAAACTTTTTAAAATAAAAAAATGCATTATTGTAATATATCT 1920 	1801 GCATTCTAGAATACATCTTTTCAAATTTCAACAAACACAGCTTTAACTTTTCTTTC	1741 GTTTGAACAATGTATGTCCGGTGTACATCTATGACCTTTCAACTCAAACTAGTGAATAAT 1800	1681 AATTTAAAATAAATTATTGAGCATGGGAAGTTCACGGGCATCATTGAGCAGCACTAGACT 1740 	1621 TGTAITCAATAGTITTAATATAAAAGTAAATTTAAATTAATTGTTATTTTTTGTTTACAGA 1680 	1561 TTATCTGAAAAGCAAATAATATCTTTGTAAAACAGCGTTCGGTCAAATGGGAAGTTCATG 1620 	1501 CTGATTAGTCGATTACCGCCTTTTATAATTTTACAATACTGAGTAATATGAATAAATCAG 1560 	1441 TAAGATTATAAATCTATGTTATAATGATAATATAATTTAAAAATAATAATACTATATTAAAT 1500 		1321 AGAAAGTTTTGAAATGTATAGAATTGAGTGGGACATCCATRAAAGGAAAGTGTATAGAAT 1380 		AAAG      AAAG	

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Qy 541 TGGCCGAATGCTTCTCAAAATGTTTTTTATATGTAAAATAATGCCCATCCAAGGATAAGT 600	Db 421 aggacgacittaggigaatacacatigtagigigigigigigigigigigigigigigigigi	361 CCGTCTTCCAAGATAATATATTTTAATTTTGTAGCCTCCCTTTTAACCAAATTCGCATGC 42	Qy 241 AACGGCCTCAATAAAAGATCATTCATAAATGTATCTTTCAATTTTAGGATAACAATACGT 300	Qy 121 TACTAACTTCTCTCCAACTTCTCTTTCCAAACACTTTATTA	Db 1 ĠĀſĠŦĠŦĠĊĠŦĀĠĀĠĊĀĠĀŔĠĠĊĠŦŦŢĠĠŦŤŢĠĀĠĀĠĀĠĠĀĠĀĀĠĊŦĠĊŦŦĊŦĠĀ 60  Qy 61 CTŢĊŢŢŢŢŢŢŢŢŢŢĠĀĊĊŢĠŢŢŢĠŢĀŢĀĀĀĀĠĀĀĠŢĀĠĀĀĠŢŢŢŢĀĀĀĀĀĠĊŢĠĊĠĀĀ 120	0	BS	PD 20-JUN-2000 PP 01-OCT-1999 JP 1999281475 PR PI SATOMI NISHIKAWA,KENJI OEDA PC C12N15/09,A01H5/00,C12N1/21,C12N5/10/(C12N5/10,C12R1:91), PC C12N15/00, PC C12N5/00,(C12N5/00,C12R1:91) CC C12N5/00,(C12N5/00,C12R1:91)	Unclassified.  REFERENCE 1 (bases 1 to 2052) AUTHORS Nishikawa, S. and Oeda, K. TITLE Plant promoter and terminator PALENCE: JP 2000166577-A 7 20-JUN-2000; SUMITOMO CHEM CO LTD OS Daucus carota L. PN JP 2000166577-A/7
1621 TGTATTCAATAGTTTTAATATAAAAGTTAAATTTTAAATTGTTAATTTTTT	1561 TTATCTGAAAAGCAAATAATATCTTTGTAAAAACAGCGTTCGGTCAAATGGGAAGTTCATG	Oy 1441 TAAGATTATAAATCTATGTTATAATGATAATATATATATA	Oy 1321 AGAAAGTTTIGAAATGTATAGAATTGAGTGGGACATCCATAAAAGAAGTGTATAGAAT 1380  Db 1321 AGAAAGTTTTGAAATGTATAGAATTGAGTGGGACATCCATAAAAGGAAAGTGTATAGAAT 1380  Db 1321 TAAATGGGACAGAGGGAGTAATACCTTTATGATATAAATTTTTGTTATTTGATTTCA 1440  Oy 1381 TAAATGGGACAGAGGGAGTAATACCTTTATGATATAAATTTTTGTTATTTTGATTTCA 1440  Db 1381 TAAATGGGACAGAGGGAGTAATACCTTTATGATATAAATTTTTTGTTATTTTGATTTCA 1440	1201 AAAGAAAAGAGAAAAGTGGGTAAAGTAGGGGGACCCACCAATATTAAATTGATAGATTTAG 1201 AAAAGTAGTTGAAAAGTAGGGGTAAAGTAGGACCCACCAATATTAATTGATAGATTTAG 1261 AAAAGTAGTTGAAAGTAGTGGGTGGGTGGGTTGTTTTTTT	1141 ATACATATGGATTGGACACGGAGACTAAGAAAAATGTATAAAGTAATGTAGAGTAAAAAG	Qy 1021 TGATCATCCATTAAAACCTTGTTAAAACAAATTCAATGAGATAAAATATCTTACAATGAA 1080	Qy 901 TAAACTGATCTAAAGCACATAGAAATTTAGTACAGGTTAAAACTTTTACAAGAATTTATA 960	Oy 781 ATTAGACTATTAATTAAGTTACTAATAAAGAAGAGTTAGTT	661 AATACTTTTAGACGACAAGAGACTTAGGTCAAAAATGGACGCTGGTAAACAGCCTAGACT

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Plant promoter and terminator.
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E40090.1 GI:18627206
JP 2000166577-A/4.
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unidentified
1 (bases 1 to 2048)
Nishikawa,S. and Oeda,K.
Plant promoter and terminator
Patent: JP 2000166577-A 4 20-JUN-2000;
SUMITOMO CHEM CO LTD
OS Daucus carota L.
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PD 20-JUN-2000
PF 01-OCT-1999 JP 1999281475
PR SATOMI NISHIKAWA, KENJI OEDA
PC C12N15/09, A01H5/09, C12N1/21, C1
C12N15/00, (C12N5/00, C12R1:91)
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/db_xref="taxon:32644"
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Torikal, S. and Oeda, K.
Plant promoter and utilization thereof
Patent: US 5959176-A 2 28-SEP-1999; —
Location Dualifiers
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Sequence 2
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Unclassified.
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patent US 5959176.
Score 241.2; DB 6
Pred. No. 3.7e-28;
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AUTHORS

TOTIKAI, T. and Oita, K.

VEGETABLE PROMOTER AND ITS USE

JOURNAL

PATENT: JP 1998052273-A 2 24-FEB-1998;

SUMITOMO CHEM CO LID

OS Daucus carota L. (carrot)

PN JP 1998052273-A/2

PD 24-FEB-1998

PF 12-AUG-1996 JP 1996212680

PI TORIKAI TOSHIMI, OITA KENJI

PC C12N15/09,A01H5/00,C07H21/04,C07K14/415,C12N1/21,C12N5/10; CC

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                         /organism="unidentified"
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Best Local Similarity 72.8
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Torikai,S. and Oeda,K.
Plant promoter and utilization thereof
Patent: US 5959176.A 1 28-SEP-1999,
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTCTTTCAACGGATTGGAATCCTTTTCTAAACTTTTTAAAATAAAAAAATGCATTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAGTGAAT-AATGCATTCTAGAATACATCTTTTCAAATTTCAACAACACAGCTTTAACT
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                                                                                                9.6%;
nilarity 89.6%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTGTTTCAGAAATTTAAATTAAATTATTGAGCATGGGAAGTTCACGGGCATCATTGAGC
                                                                                                                                                                   /organism="unknown"
/mol_type="unassigned
                                                                                                                                                                                                                                                                                                                                                          from
                                                                                                                                                                                                                                                                                                                               GI:10003562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.8%;
                                                                                                                                                                                                                                                                                                                                                          patent US
                                                                                             Score 196.6; DB 6;
Pred. No. 4.9e-21;
0; Mismatches 24;
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Pred. No. 3.7e-28;
0; Mismatches 128;
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S 5959176.
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1958 1968 1898

1908

1840 1848 1780 1789

2018

30-AUG-2000

RESULT 7
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SOURCE
ORGANISM

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FEATURES

Gaps

source

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LABBITIED

1 (bases 1 to 247)

1 (bases 1 to 247)

TOTIAL TOTIAL, T. and Olta, K.

TITLE

VEGETABLE PROMOTER AND ITS USE

PATOMO CHEM CO LTD

OS Daucus carota L. (carrot)

PN UP 1998052273-A/1

PD 24-FEB-1998

PP 12-AUG-1996 UP 1996212680

PI TORIKAI TOSHIMI, OITA KENJI

PC C12N15/09, A01H5/00, C07H21/04, C07K14/415, C12N1/21, C12N5/10; CC

Strandedness: Single;

CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
PH Key

FT Source

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                                                                                                               ACCTCAACATTGATGTTAGCGTACTATAAATAGGTGCTCTTGGTGCTCTACCATCATCAC 1983
                                                                                                                                                                                                                                      TGGAATCCTTTTCTAAACTTTTTAAAATAAAAAAATGCATTATTGTAATATTTATCAAC
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                                                                                                                                                                                                                                                                                                                          CTAAAGGTC 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                       9.6%;
nilarity 89.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Pred. No. 4.9e-21;
0; Mismatches 24;
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RESULT 10
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KEYWORDS
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ORGANISM
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E55065
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                                                                                                                   JOURNAL
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           Plant promoter
Patent: JP 2000083679-A 2 28-MAR-2000;
SUMITOMO CHEM CO LTD
OS Daucus carota L.
PN JP 2000083679-A/2
PD 28-MAR-2000
PF 12-JUL-1999 JP 1999197240
PR
PI IKUHARU ISHIGE, SATOMI NISHIKAWA, KENG
PC C12N15/09, A01H5/00, C12N1/21, C12N5/10
                                                                                                                                                                                                                                                                                                                                                           2045
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                                                                                                                                           unclassified.
1 (bases 1 to 246)
1 shige, I., Nishikawa, S. and Oeda, K.
                                                                                                                                                                                      unidentified
                                                                                                                                                                                                            Plant promoter.
E55065
E55065.1 GI:18625251
JP 2000083679-A/2.
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Ishige, F., Nishikawa, S. and Oeda, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unknown
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                                                                                                                                                                                                  unidentified
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IKUHARU ISHIGE, SATOMI NISHIKAWA, KENJI OEDA
C12N15/09, A01H5/00, C12N1/21, C12N5/10//(C12N15/09, C12R1:91), PC
(C12N5/10, C12R1:91), C12N15/00, C12N5/00, (C12N15/00, C12R1:91), PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.5%;
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patent US 6218598.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119
                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (27-JAN-1999) A. Sturm,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecular characterisation and functional analysis of sucrose-cleaving enzymes in carrot (Daucus carota L.) J. Exp. Bot. 47, 1187-1192 (1996)
                                                                                                                                                                                                                                                                                                            Maulbeerstr. 66, CH-4058 Basel, Related sequence X67163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; asterids; campanulids; Apiales; Apiaceae; Apioideae; Scandiceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    beta-fructofuranosidase; Inv*Dc5 gene; invertase; isoform
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Y18706
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CC
FH Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCAATCTTACACCACAAACCTTGAGCTTAATTTTCTACTTATTCTCAGCAATAACATTC
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                   /gene="Inv*Dc5"
join(2767. .3160,3724. .3732,4656. .5515,5605. .5766,
5869. .6104,6190. .6277,6384. .6587)
                                                                                                                                                                                           /organism="Daucus carota"
/mol_type="genomic DNA"
/cultivar="Nantaise"
                                                                                                                                                                   'B
                                                                                                                          gene="Inv*Dc5"
                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism='Daucus carota L.'.
                                                                                                         .2666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                    8005
                                                                                                                                                                        xref="taxon:4039"
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Pred. No. 7e-21;
0; Mismatches :
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SWITZERLAND
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17
                                             CACTATGGGGGTTTTTTTTTTCCCGGAAGTAGGAGCTGCTTCCGTCTTCTGCTTTGA
                                                                                        CACATAGGGCCTGTTTGGTTGAGAGAAGCAGAAGCTGCTTCTGACTTCTTCTTCTTTGA
                                                                                                                                                8.5%; Score 174; DB 8; Length 8005; ilarity 81.7%; Pred. No. 8.2e-18; Conservative 0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="beta-fructofuranosidase, isoform II"
/protein id="ca477266.1"
/protein id="Ca477266.1"
/db_xref="di:4454115"
/db_xref="di:4454115"
/db_xref="di:4454115"
/db_xref="di:4454115"
/db_xref="di:4454115"
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/db_xref="miniprot/Tremal:042722"
/db_xref="miniprot/Tremal:042722"
/translation="mamplification-"mampledegaptyVapargvapagoserrapinasevov
/translation="mamplification-"mampledegaptyVapargvapagosevov
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/dlayzapapsdpilliewrypagosevov
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/gene="Inv*Dc5"
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/gene="Inv*Dc5"
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ARIIASLNIWQMYTAQRQTHFADLVI"
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gene="Inv*Dc5"
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|gene="Inv*Dc5"
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/EC_number="3.2.1.26"
/note="soluble_acid_invertase"
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VERSION KEYWORDS SOURCE

ACCESSION

FOCUS

RESULT 12

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Best Local Similarity 82.5%;
Matches 198; Conservative
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                                                                                                                          TTCTGCTTCTTTTCCAAACACTTTATCAACTTACCTACTTCTCACTTCTCTCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAY-2001 JP 2001164069
SATOMI NISHIKAWA, KENJI OEDA
C12N15/09,A01H5/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/
             and use thereof.
                                                                                                                                                                                                                                                                                                                      /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Pred. No. 6.4e-16;
0; Mismatches 41;
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DARGCHS2
LOCUS
DEFINITION
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Best Local Similarity
Matches 198; Conserv
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Direct Submission

Direct Submission

Submitted (14-MAY-1993) Yoshihiro Ozeki, College of Arts and Sciences, The University of Tokyo, Department of Biology; Kor Meguro-ku, Tokyo 153, Japan (Tel:03-3467-1171(ex.253),
                                                                            1 (bases 1 to 4886)
Ozeki, Y., Davies, E. and Takeda, J.
Structure and expression of chalcone synthase suspension cultured cells regulated by 2,4-D plant Cell Physiol. 34, 1029-1037 (1993)
                                                                                                                                                                                chalcone synthase.
Daucus carota (carrot)
Daucus carota
                                                                                                                                                                                                                  DARGCHS2 DARGCHS2 gene for chalcone synthase.
D16255
D16255.1 GI:441168
                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Apiales; Apiaceae; Apioideae; Scandiceae;
                                                         Ozeki,Y.
                                                                                                                                     Daucinae; Daucus
                                                                   2 (bases 1 to
                                                                                                                                                                                                                                                                                                                          TTGCTATAAGCAAGAAATCACTTCTTTTAAGCTAACCCAAACGGCCTCAATAAAAGATCA 261
                                                                                                                                                                                                                                                                                                                                                                       TTCCGCTTCTTTCCAAACACTTTATTAACTTTTTTACTTCTCATTTCTACTCCACTTCT 201
                                                                                                                                                                                                                                                                                                                                                                                                                       AGGGCCTGTTTGTTTTATGGAATCAGAAGCTGCTTCTGACTTCTGCTTTTTTT-ACCCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SATOMI NISHIKAWA, KENJI OEDA
C12N15/09, A01H5/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="unidentified"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.9%;
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Pred. No. 6.4e-16;
0; Mismatches 41;
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1535 TACTCCACTTCTTTAATTTAAGCAAGAAGTCACTTCTTTTAAACTAACCCAAACCGCCC 1594
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                      190 TACTCCACTTCTTTGCTATAAGCAAGAATCACTTCTTTTAAGCTAACCCAAACGGCCTC 249
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                                                                                                                                                                                                                                                 11 CTACAGCACATAGGGCCTGTTTGGTTGAGAGAGAGGAGAGGTGCTTCTTGACTTCTTCTTC 70
                                                                                                                                                                          TTTTGACCTGTTTGTATAAAGAAGTAGAAATATTTTTAAAAAGCTGGGAATACTAACTTC 130
                                                                          rcicicagageticigitititititiceaaacacitiaticatitatitatitaetiteeetic
                                                                                                  TCTCTCACAACTTCCG-CTTCTTTTCCAAACACTTTATTAACTTTTTTTACTTCTCATTTC 189
                                                                                                                                                TCTTGACCCGTTTGGGTÄÄÄGÄÄGTÄGÄÄGGÄCTTTTÄÄGÄÄGTTGAGÄÄTÄCTÄGCTTC 1474
                                                                                                                                                                                                                           CTAGTAGATGTÁGGGCCTGTTTGGATGGTGGAAGCAGAAGCTGCTTCCGGCTTCTGCTTT 1414
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Arts & Science, Univ. of Tokyo
3-8-1 Komaba, Meguro-ku
Tokyo 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (14-MAY-1993) to DDBJ Yoshihiro Ozeki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Godon start= 1
/ product="chalcone synthase"
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2327. 2331
2358. 4519
/note="CHS2 mRNA and intron"
2358. 2607
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03-3485-2904.
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join(2430. .2607 arr.
/gene="rr...
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Search completed: March 15, 2005, 13:22:00 Job time: 8943.89 secs

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Gapop 10.0 , Gapext 1.0
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Listing
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  118388833
         ADP07499
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AAV15143
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                                                                                    Aav15143 New promo
Aaz49611 Carrot CR
Adp07499 Carrot DN
Adc56759 Carrot DN
Adc56761 Carrot DN
                            Aaz49615
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Abz101046
Aaa37960
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Aav15143
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         Abz10100 Haematopo
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Carrot te
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Ads89551 Oligonucl	ADS89551	13	5286	3.3	67.4	45		
Abl34011 Human imm	ABL34011	0	6050		67.6	44		
Abq66994 Human ang	ABQ66994	σ	5984		67.6	43		
Abd32992 Human can	ABD32992	13	99764		67.8	42	a	
Abk28233 DNA trans	ABK28233	σ	15732	3.3	67.8	41	a	
Aas45388 Chemicall	AAS45388	4	15732		67.8	40	Ω	
Abl32218 Human imm	ABL32218	σ	11422		68	39		
Abk39936 Human che	ABK39936	σ	11422		68	38		
6 Continuation (7 of	ABD32968_	13	110000	3.3	68.2			
Abl34155 Human imm	ABL34155	σ	15548		68.2	36	a	
Abl70624 Chemicall	ABL70624	ტ	6045		69.2			
Abk31541 Signal tr	ABK31541	0	6045		69.2	3 4		
Abl70376 Chemicall	ABL70376	σ	16258		69.4	33	ი	
Abk40038 Human che	ABK40038	6	16258		69.4	32	a	
Adb54190 Pretreate	ADB54190	10	11222		69.6	31	ი	
Acf62794 Colon can	ACF62794	8	8222		69.6	ω O	Ω	
Aas61235 Human gen	AAS61235	6	6352		69.8	29		
Abl70563 Chemicall	ABL70563	0	6352	3.4	69.8	28		
Abk31340 Signal tr	ABK31340	6	6352		69.8	27		
Ads89552 Oligonucl	ADS89552	13	5286		70.8	26	ი	
Ads89278 Oligonucl	ADS89278	13	5286		70.8	25	O	
Abl32517 Human imm	ABL32517	თ	5930		71	24	a	
Adb54318 Pretreate	ADB54318	10	11222		71.2	23	a	
Acf62816 Colon can	ACF62816	8	8222		71.2	22	a	
Abk28332 DNA trans	ABK28332	σ	11745	3.7	75	21	a	

## ALIGNMENTS

RESULT 1
AAA37959
ID AAA37959
ID AAA37959
ID AAA37959
ID AAA37959
ID AAA3
AC AAA3
AC AAA3
AC CAY
XX CAY
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CCC ter Nishikawa S, Carrot; promoter; terminator; transgenic plant; breeding; fertility; ds. AAA37959; 02-OCT-1998; 28-SEP-1999; WO200020613-A1 Daucus carota. Carrot promoter sequence 18-AUG-2000 AAA37959 standard; DNA; 2052 (SUMO ) SUMITOMO CHEM CO LTD. (first entry) Oeda K; 98JP-00281124. 99WO-JP005303. #1. ΒP

This sequence represents a carrot promoter. The invention relates to plant promoters and terminators from Daucus carota L. which are capable of expressing a gene of interest in plants. The invention also includes a chimeric gene characterized in that it comprises the promoter and a desired gene linked to each other in the form capable of functioning. A method of producing a transformant comprises introducing the promoter, the chimeric gene or a vector comprising the promoter and a desired gene or a vector comprising the promoter and a desired gene or terminator sequence into a host cell. The plant promoters and terminators are useful in plant breeding, for e.g. fertilities of plants may be controlled by expressing, in the host cells, a sense or antisense

New Plant promoters and terminators from Daucus carota  $L_{\cdot,\cdot}$  useful plant breeding, for e.g. controlling fertilities of plants.

WPI; 2000-303791/26.

Claim 1; Page 69-70; 81pp; English.

odg 1

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Gene of a male sterility related gene such as 5-locus-specific RNase gene Sequence 2052 BP; 737 A; 317 C; 316 G; 682 T; 0 U; 0 Other; probabilistic probabil	
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1021 TRANCONAMICATITINANCINGTUTURANCANTICATITICATITICALITACIA 1200 1021 TRATCATCCATTANACCITITITINANCIANTICACITACIAN 1000 1021 ANAGRACIANTATICATITITINANCIANTICACITACIAN 1000 1021 ANAGRACIANTATICATITICANANCIANTICACITACIANCIAN 1000 1021 ANAGRACIANTATICATITICANATATICATITICATITICALITA 1200 1141 ATRICATATICANTICACITITITINANCIANTICACITACIANTATICATITICATITICA 1200 1141 ATRICATATICANTICACITICATITICATITICA 1200 1141 ATRICATATICANTICACITICATITICATITICA 1200 1141 ATRICATATICANTICATICATICATICATICATICATICATICATICATITICA 1200 1141 ATRICATATICANTICATICATICATICATICATICATICATICATICATICA	

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Best Local Similarity
                                                                                                                                                                                                                                                                Matches 2050; Conservative
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                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 78-79; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nishikawa S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant promoters and terminators from Daucus carota L., nt breeding, for e.g. controlling fertilities of plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMITOMO CHEM CO
                                                                                                                                                                                                                            CATGTGTGCCCTACAGCACATAGGGCCTGTTTGGTTGAGAGAGCAGAAGCTGCTTCTGA
                                                                                                                  TACTAACTTCTCTCTCACAACTTCCGCTTCTTTTTCCAAACACTTTATTAACTTTTTTACT
                                                                                                                                                                     CTTCTTCTTTTGACCTGTTTGTATAAAGAAGTAGAAATATTTTTAAAAAGCTGCGAA
                                                                                                                                                                                                                                                                                                                2052 BP; 736 A; 318 C; 317 G; 681 T; 0 U; 0 Other;
               AACGGCCTCAATAAAAGATCATTCATAAATGTATCTTTCAATTTTTAGGATAACAATACGT
                                                               TCTCATTTCTACTCCACTTCTTTGCTATAAGCAAGAAATCACTTCTTTTAAGCTAACCCA
                                                                                                                                                                                                           CATGTGTGCCCTACAGCACATAGGGCCTGTTTGGTTGAGAGAAGCAGAAGCTGCTTCTGA
AACGGCCTCAATAAAAGATCATTCATAAATGTATCTTTCAATTTTAGGATAACAATACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTCTAAATATC 2052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98JP-00281124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-JP005303.
                                                CTACTCCACTTCTTTGCTATAAGCAAGAAATCACTTCTTTTAAGCTAACCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     terminator; transgenic plant; breeding; fertility;
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RESULT 4
AAA37962
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AC CA WO200020613-A1 Carrot; promoter; Plasmid #1 DNA sequence used 18-AUG-2000 AAA37962; AAA37962 13-APR-2000. Daucus carota. standard; (first terminator; transgenic plant; breeding; fertility; ds. DNA; entry) 2048 ВÞ in mutation of promoter sequence

New Plant promoters and terminators from Daucus carota L., useful plant breeding, for e.g. controlling fertilities of plants. WPI; 2000-303791/26 Nishikawa (SUMO ) SUMITOMO CHEM တ 0eda ζ. ဗ GLT

8; Page 71-73;

81pp; English.

in

02-OCT-1998;

98JP-00281124 99WO-JP005303

28-SEP-1999;

This sequence represents a plasmid sequence used in a method for introducing a mutation into a carrot promoter. The invention relates to plant promoters and terminators from Daucus carota L. which are capable of expressing a gene of interest in plants. The invention also includes a chimeric gene characterized in that it comprises the promoter and a desired gene linked to each other in the form capable of functioning. A method of producing a transformant comprises introducing the promoter, the chimeric gene or a vector comprising the promoter and a desired gene or terminator sequence into a host cell. The plant promoters and terminators are useful in plant breeding, for e.g. fertilities of plants may be controlled by expressing, in the host cells, a sense or antisense gene of a male sterility related gene such as S-locus-specific RNase gene RNase gene 9

Sequence 2048 BP; 735 A; 317 C; 316 G; 680 T; 0 U; 0 Other;

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Query Match Best Local Similarity 99.0**%**; 99.7**%**; Score 2030.8; Pred. No. 0; DΒ u T Length 2048;

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37963 standard; DNA; 2048 BP.	1977 CACATCAATCTTACACCACAAACCTTGAGCTTAATTTTTCTACTTATTCTCAGCAATCAC 2036 2041 ATTCTAAATATC 2052		1861 GATTGGAATCCTTTTCTAAACTTTTTAAAATAAAAAAAAGCATTATTGTAATATTTATC 1920	801 GCATTCTAGAATACATCTATCAACTAAGCTTCAACTGAATGAA	741 737	7 1	1621 TGTATTCAATAGTTTTAATATAAAAGTAAATTTTAAATTAATT		156	1441 TAAGATTATAAATCTATGTTATAATGATAATAATAATATTAAAAATAATACTATAATATT 1500		13		, ,, ,,		1081 AAGAAGGACAATGTCTTTTGAAAAAACAAATAGGTACTCCCTCC	

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                                GAACAGGGTTATTTTTAACGTGTCAACAAATTCTAATAATTTTACCTGGCCGGTGAACA
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                                                                                                                             Daucus carota,
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RESULT 7
AAVL5143
ID AAV1
XX AAV1
AC AAV1
XX O2-J
XX New
XX Prom
KW Prom
KW plan
XX V3
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       Daucus carota
                                                                        02-JUL-1998
                                                                                          AAV15143;
                                                                                                         AAV15143
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                                                                                                                                                    2019
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Matches 366;
Promoter; root; carrot; Kuroda Gosun; root-specific expression; plant cell; soil pathogen; improve; nutritive value; edible root plant;
                                                           New promoter used for root-specific expression in plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a novel promoter, and is isolated from the roots of carrots, cultivar Kuroda Gosun. The promoter can be used t direct root-specific expression in plant cells. Since the promoter enables expression of a desired protein in the roots of a plant, it is useful in combat against pathogenic soil fungi and pests which are difficult to kill by chemicals. It can also be used to improve the nutritive value of edible root plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2042 BP; 719 A; 356 C; 323 G; 644 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New carrot rengineering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1554 AAATCAGTTATCTGAAAAGCAAATAATATCTTTGTAAAACAGCG----TTCGGTCAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carrot root gene, promoter and terminator - useful in ineering for directing root-specific gene expression.
                                                                                                                                                                                               standard; DNA;
                                                                                                                                                                                                                                                                                                                            CTCAGCAATAACATTCTAAATATC
                                                                                                                                                                                                                                                                                                  TTTAGCAAAAACATTCTAAAGGTC
                                                                                                                                                                                                                                                                                                                                                                      CTCTĂCTĂTCĂTCĂCĂTCĂĂTCTTCCAGCĂCĂĂACCTTGĂGCTTĂĂTCTTTCTĂCATĂAT
                                                                                                                                                                                                                                                                                                                                                                                                CTCTACTATCATCACATCAATCTTACACCACAAACCTTGAGCTTAATTTTTCTACTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATAATATTTATCAACACCTCAACATTCATGTTAGCGTACTATAAATAGGTGCTCTTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTAATATTTATCAACACCTCAACATTGATGTTAGCGTACTATAAATAGGTGCTCTTGGTG 1968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 72.6
66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTCTTTTAACAGATTAGAATOGTTTCGTAAACTTTTAAAATT--AAAAATACATTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TÁGCCÁGTGAÁTĠCTŤŤĊŤÁĠÁÁŤÁTÁŤCŤŤŤTGAÁÁŤŤŤCÁÁCÁAÁČÁČÁGČACŤÁÁĊŤ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACGTTGTATTGTTTAAACAACGTTTGTCCGGTGTATATTTATGACCTTTCAACTCAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCACTAGACTGTTTGAACAATGTATGTCCGGTGTACATCTATGACCTTTCAACTCAAAC
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                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.7%;
72.6%;
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Pred. No. 8.7e-35;
0; Mismatches 129
                                                                                                                                                                                                                                                                                               2042
                                                                                                                                                                                                                                                                                                                                       2052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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RESULT 8
AAZ49611
ID AAZ4
XX AAZ4
XX AAZ4
XX AAZ4
XX O7-A
XX Carr
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KW Synt
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 223;
                                                                                     Synthetic DNA; plant promoter; CR16.3 fragment; soybean glycinin; stearoyl-ACP-desaturase gene; male sterility-related gene; ds.
                                                          Daucus carota.
                                                                                                                                                   Carrot CR16.3
                                                                                                                                                                               07-APR-2000
                                                                                                                                                                                                                                           AAZ49611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 247 BP; 88 A; 50 C; 21 G; 88 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the roots of carrots, cultivar Kuroda Gosun. The promoter can be used to direct root-specific expression in plant cells. Since the promoter enables expression of a desired protein in the rod specific tissusseful in combat against pathogenic soil fungi and pests which are difficult to kill by chemicals. It can also be used to improve the nutritive value of edible root plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New carrot root gene, promoter and terminator - useful in engineering for directing root-specific gene expression.
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                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGAATCCTTTTCTAAACTTTTTAAAATAAAAAAAATGCATTATTGTAATATTTATCAAC 1923
                                                                                                                                                                                                                                                                                                                                                                                                          ATCAATCTTACACCACAAACCTTGAGCTTAATTTTTCTACTTATTCTCAGCAATAACATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCTCAACATTGATGTTAGCGTACTATAAATAGGTGCTCTTGGTGCTCTACTATCATCAC 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCTAGAATATATCTTTTGAAATTTCAACAAACACAGCACTAACTTTTCTTTTAACAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 14; 31pp;
                                                                                                                                                                                                                                                                                                                      CTANAGGTC 247
                                                                                                                                                                                                                                                                                                                                                 CTAAATATC 2052
                                                                                                                                                                                                                                                                                                                                                                                ATCAATCTTCCAGCACAAACCTTGAGCTTAATCTTTCTACTAATTTTTAGCAAAAACATT
                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCTCAACATTCATGTTAGCGTACTATAAATAGGTGCTCTTGGTGCTCTACTATCATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAGAATCGTTTCCTAAACTTTTAAAATT--AAAAATACATTACTATAATATTTATCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oeda K;
                                                                                                                                                                               (first entry)
                                                                                                                                                 fragment for synthesis of plant promoter.
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                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.6%;
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                                                                                                                                                                                                                                           246 BP
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Pred. No. 5.8e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24;
                                                                                                                     carrot;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                   transgenic
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                                                                                                                   plant;
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RESULT 9
ADPO7499
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XX ADPO
XX ADPO
XX ADPO
XX ADPO
XX Carr
XX Carr
XX Carr
XX Carr
XX Carr
XX Carr
XX Dauc
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Best Local Similarity
Matches 222; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is a CR16.3 fragment from carrot genomic DNA. It is used for synthesis of a plant promoter which comprises nucleotides 112-246, 54-246, or 1-246 of this sequence and a synthetic DNA. The promoter is used for controlling the expression of a desired gene e.g. soybean glycinin, stearoyl-ACP-desaturase and S-locus type specific RNase gene (male sterility-related gene) in a host cell especially a microorganism or a plant cell. The transformed plant cells can be used to produce transgenic plants. The promoter is compact and therefore suitable for higher expression of a desired gene in a particular tissue compared to the promoter transgenic plants.
                                                                                              Carrot; gene; transcription
                                          JP2004135597-A
                                                                                                                                             Carrot DNA
                                                                                                                                                                      29-JUL-2004
                                                                                                                                                                                                   ADP07499;
                                                                                                                                                                                                                               ADP07499 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 246 BP; 88 A; 50 C; 21 G; 87 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 11-12; 24pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1865 GGAATCCTTTTCTAAACTTTTTAAAATAAAAAAAATGCATTATTGTAATATTTTATCAACA 1924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    host tissues
                                                                     carota.
                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTCAACATTGATGTTAGCGTACTATAAATAGGTGCTCTTGGTGCTCTACTATCACA 1984
                                                                                                                                                                                                                                                                                                                               TAAATATC 2052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAATCGTTTCCTAAACTTTTAAAATT--AAAAAATACATTACTATAATATTTATCAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                      CCTCAACATTCATGTTAGCGTACTATAAATAGGTGCTCTTGGTGCTCTACTATCATCACA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTAGAATATATCTTTTGAAATTTCAACAAACACAGCACTAACTTTTCTTTTAACAGATT
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                                                                                                                                                                      (first
                                                                                                ds; expression inducing promoter;
start point; RNA polymerase II.
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                                                                                                                                                                                                                               DNA; 196 BP
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Pred. No. 8.9
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13-MAY-2004

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RESULT 10
ADC56759
XX ADC56
XX ADC56
XX ADC56
XX ADC56
XX Carro
XX Carro
XX Carro
XX Carro
XX Daucu
XX Daucu
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Best Local Similarity
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                      WPI; 2003-472920/45
                                                                                                                                                         31-MAY-2001; 2001JP-00164069
                                                                                                             31-MAY-2001; 2001JP-00164069
                                                                                                                                                                                                                                                                                                          Daucus carota subsp.
                                                                                                                                                                                                                                                                                                                                                                                    carrot;
                                                                                                                                                                                                                                                                                                                                                                                                           Carrot DNA that encodes an expression inducer type promoter.
                                                                    (SUMO ) SUMITOMO CHEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC56759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADC56759 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an expression inducing promoter comprising a first DNA linked to a second DNA at its 5' terminus, where the first DNA has a region which determines a transcription start point of RNA polymerase II and has minimum promoter function, and the second DNA has expression inducing promoter function in a plant cell. The expression inducing promoter is useful for expressing a foreign gene. This sequence represents carrot DNA used in the scope of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 4; 61pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expression inducing promoter, useful for expressing foreign gene, comprising first DNA for detecting transcription start point and having minimum promoter function, linked to second DNA having expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-OCT-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTATCATCACATCAATCTTACACCACAAACCTTGAGCTTAATTTTTCTACTTATTCTCA
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                                                                                                                                                                                                                                                                                                                                                           inducer type promoter; plant; vector; transformant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA; 2831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.5%;
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Pred. No. 1.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4e-26;
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RESULT 11
ADCS6761
ID ADCS6
XX ADC56
XX ADC56
XX Carro
XX Carro
XX Carro
XX Carro
XX Daucu
XX Daucu
XX JP200
XX AT SI-MA
XX JI-MA
XX JI-MA
XX AT SI-MA
XX DISCI
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CC Promo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                          An expression in var. sativa DC.
                                                    Disclosure;
                                                                                                                                     WPI; 2003-472920/45.
                                                                                                                                                                                        31-MAY-2001; 2001JP-00164069
                                                                                                                                                                                                                 31-MAY-2001; 2001JP-00164069
                                                                                                                                                                                                                                                                        JP2003000252-A.
                                                                                                                                                                                                                                                                                                 Daucus carota subsp.
                                                                                                                                                                                                                                                                                                                                          carrot; expression
                                                                                                                                                              (SUMO ) SUMITOMO CHEM
                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                            ADC56761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC56761 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to carrot DNA used as an expression inducer type promoter. Specifically, it refers to promoter sequences derived from plant DNA, preferably carrot, and functional mutants thereof that can be used as expression inducers. Furthermore, the present invention describe DNA, vectors, transformants and the process by which to prepare transformants. This polymucleotide sequence is the DNA encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to promoter. Specifically, it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An expression inducer type promoter derived from DNA of Daucus carota var. sativa DC. of 2831 bases and its analogues having the same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGCTATAAGCAAGAAATCACTTCTTTTAAGCTAACCCAAACGGCCTCAATAAAAGATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTACTATAAGCAAGAAGTCAATTCTTTTAAATTAACCCAAACGGCCCCTAAGTAATTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCTGCTTCTTTCCAAACACTTTATCAACTTACCTACTTCTCACTTCTGCTTCACTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCCGCTTCTTTTCCAAACACTTTATTAACTTTTTTACTTCTCATTTCTACTCCACTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2831 BP; 950 A; 456 C; 395
                                                    SEQ
                                                                                                                                                                                                                                                                                                                                                          encoding an expression inducer type promoter (SeqID 3).
                                                                                   inducer type promoter derived from
C. of 2831 bases and its analogues b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                   ID NO
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                                                                                                                                                                                                                                                                                                                                                                                            entry)
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                                             3; 16pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 162.4; |
Pred. No. 1.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                      promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G; 1030 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.5e-20;
                                                                                                                                                                                                                                                                                                                                 plant; vector; transformant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
                                                                                    n DNA of Daucus
having the same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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This invention relates to carrot DNA used as an expression inducer promoter. Specifically, it refers to promoter sequences derived fro plant DNA, preferably carrot, and functional mutants thereof that c

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RESULT 12
AAZ49616/c
ID AAZ496
XX AAZ496
XX AAZ496
XX Oligon
XX Synthe
KW Synthe
KW Synthe
KW Synthe
KW Synthe
XX Daucus
OS Daucus
OS Synthe
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The present sequence is an oligonucleotide (- chain) used to prepare a CR16.1 DNA fragment comprising nucleotides 112-246 of the carrot CR16.3 fragment. The CR16.1 DNA fragment is ligated to a 10 bp synthetic DNA for construction of a plant promoter. The promoter is used for controlling the expression of a desired gene e.g. soybean glycinin, stearoyl-ACP-desaturase and S-locus type specific RNase gene (male sterility-related gene) in a host cell especially a microorganism or a plant cell. The promoter is compact and therefore suitable for higher expression of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic DNA; plant promoter; CR16.1 fragment; carrot; trasoybean glycinin; oligonucleotide; stearoyl-ACP-desaturase male sterility-related gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used
                                                                                                                                                                                                                                                                                                                                      Novel promoter used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA, vectors, transformants and the process by which to prepare transformants. This polynucleotide sequence is DNA encoding a carrot promoter (SeqID 3) of the invention.
                                                                                                                                                                                                                                                               Disclosure; Page 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Daucus carota.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide-4 for synthesis of CR16.1 fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMITOMO CHEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGGCCTGTTTGGTTGAGAAGAAGCAGAAGCTGCTTCTGACTTCTTCTTCTTTTTGACCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCCGCTTCTTTTCCAAACACTTTATTAACTTTTTTACTTCTCATTTCTACTCCACTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Nishikawa
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                                                                                                                                                                                                                                                                                                                 gene.
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82.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                         plants with higher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carrot; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 125;
                                  The present sequence is an oligonucleotide (+ chain) used to prepare a CR16.1 DNA fragment comprising nucleotides 112-246 of the carrot CR16.3 fragment. The CR16.1 DNA fragment is ligated to a 10 bp synthetic DNA for construction of a plant promoter. The promoter is used for controlling the expression of a desired gene e.g. soybean glycinin, stearcyl-ACP-desaturase and S-locus type specific RNase gene (male sterility-related gene) in a host cell especially a microorganism or a plant cell. The transformed plant cells can be used to produce transgenic plants. The promoter is compact and therefore suitable for higher expression of a promoter is compact and therefore suitable for higher expression of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic DNA; plant promoter; CR16.1 fragment; carrot; trasoybean glycinin; oligonucleotide; stearoyl-ACP-desaturase male sterility-related gene; ss.
                                                                                                                                                                   Disclosure; Page 13; 24pp; English.
                                                                                                                                                                                             of a
                                                                                                                                                                                                                                                                                                                                                               02-FEB-2000.
                                                                                                                                                                                                                                                                                                                                                                                         EP976832-A2
                                                                                                                                                                                                                                                                                                                                                                                                                 Daucus carota.
Synthetic.
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                          desired
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                                                                                                                                                                                                                                                                                                            15-JUL-1998;
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                                                                                                                                                                                                                                                                                    (SUMO)
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                                                                                                                                                                                                                                                           Nishikawa
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                                                                                                                                                                                                                                                                                                                                       99EP-00113732.
                                                                                                                                                                                                                                                                                    CHEM CO
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                         particular tissue compared
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       particular tissue compared to other host tissues
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92.6%;
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                                                                                                                                                                                                         produce transgenic plants with higher expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CR16.1 fragment for
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                          to other host tissues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plant promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene,
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Query Match Best Local Similarity Matches 125; Conserv

5.8%; nilarity 92.6%; Conservative

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Score 119; DB 3; Pred. No. 1.1e-12; 0; Mismatches 10

10;

Indels

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0

Length

Sequence

140

BP;

44

A; 34 C; 17 G;

45 T; 0 U; 0 Other;

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rtgrtgaaaaaaaraaaaarrtgaaaargaaaaaaaargtaa 2925
                            GTTATAATGATAATATAATTTTAAAAATAATACTATATTTAATTC 1501
                                                                         TAATGATATTT -- TTTATAAAATATTAAAAATTTGAAATTAT
                                                                                                   GTAATACCTTTATGATATAAATTTTTGTTTATTTTGATTTCAT 1441
                                                                                                                                                                                   ATAGAATTGAGTGGGACATCCATAAAAGGAAAGTGTATAGAATT 1381
                                                                                                                                                                                                                                                              GTGGGTGGGTGGGATTTTTATATTTATAAAAATTTTACTATTTTGA 1321
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РСТААТАЛАТАЛАБАБАБАТТАБТАЛА, САБАЛАДБЕТАЛАЛА, В 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTTAGGTCAAAAATGGACGCTGGTAAACAGCCTAGACTTGGTCAC 727
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                                                                                                                                                TTAATTGTTTATTTTTAATAAATTTÄÄATGAATTTTGTTTATTA 2807
                                                                                                                                                                                                                                                                                                  GGTAAAGTAGCGGGACCCACCAATATATATTGATAGATTTAGA 1261
                                                                                                                                                                                                                                                                                                                                                                                                              CACGGAGACTAAGAAAATGTATAAAGTAATGTAGAGTAAAAAAAGA 1201
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                                                                                                                                                                                                                           TTTTTTTAATAAAATAATTTGTTAAATAAAT----TATTAATA 2747
                                                                                                                                                                                                                                                                                                                                                                              TTTATTTTTÄAÄAAATTTTATTAÄAÄÄÄTÄTTTTÄAATATTÄTÄAAT 2094
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Pred. No. 7.2e-09;
0; Mismatches 761; Indels 18;
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AC ABZIO
XX 16-JA
XX Hamar
XX Hamar
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XX Homo
XX Homo
XX Gree
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                                                                      Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent tidistinguishes between methylated and non-methylated CpG dinucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
                                   Claim 28; SEQ ID NO 240; 117pp; English.
                                                                                                                                                     WPI; 2003-018942/01
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 present invention describes a method for detecting
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which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118 crepresent specifically claimed nucleotide sequences from the present creation. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative clisorder haematopoietic cells; for differentiating between acute [CC] lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide collymorphisms (SNPs) of haematopoietic cell proliferation disorder crelated sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent,
disorders allowing for improved and informed treatment of patients
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Sequence 8056 BP; 3711 A; 371 C; 371 G; 3603 T; 0 U; 0 Other;

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Matches 627; Conserv 1478 1538 1418 847 727 547 GCTATTAATTAAGTTACTAATAAATAAGAGAGGTTAGTAAACAGAAAGCAGGTAAAAACA 846 CCCGTTTAACCAGTTTGTTAATATATATGTTTACACTTACAAGAGGATATTCGTAATACT AGAGCTTGCTGCTGTGTTAGTTGTTGTGAGCTCATTTCTTTAAAAGTAATGTAAACT 906 TAATTTTÄATATTTTÄAAAAAATCGAAATAAACGAATCGTAAAATTAAAAAAATTATTTT CTGATAAATAGATAATTGTTAGTATAATATAGTAGGATCTACAATGACATTAAAATTAGA 786 TTTAGACGACAAGAGACTTAGGTCAAAAATGGACGCTGGTAAACAGCCTAGACTTGGTCA AATGCTTCTCAAAATGTTTTTTATATGTAAAATAATGCCCATCCAAGGATAAGTAAAATT Conservative 44.2%; . Score 91.8; Pred. No. 1. Mismatches 767; 8; DB 8; 1.8e-07; Indels 25; Gaps 1417 1537 726 666 909 5

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ATGGATTGGACACGGAGACTAAGAAAATGTATAAAGTAATGTAGAGTAAAAAAGAAGAG 1206 

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--AAGAAAAGTGGGTAAAGTAGCGGGACCCACCAATATATAATTGATAGAT 1256

TCCATTAAAACCTTGTTAAAACAAATTCAATGAGATAAAATATCTTACAATGAAAAGAAG GATCTAAAGCACATAGAAATTTAGTACAGGTTAAAACTTTTACAAGAATTTATATTAAAC 966

GAAAATCATTTTATAACATGTCTCTCGGCTGTCATTATAATAGGGATCACTTACTGATCA

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Search completed: March 15, 2005, 10:51:21 Job time: 1109.24 secs

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## ALIGNMENTS

REFERENCE AUTHORS TITLE RESULT 1 CNS00EVL/c ORIGIN SOURCE ORGANISM FEATURES COMMENT KEYWORDS VERSION DEFINITION ACCESSION JOURNAL source Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Marron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm. fly), ger AL069706 CNSODEVL 1101 bp DNA linear GSS 04-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC: BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. Drosophila melanogaster (fruit fly)
Drosophila melanogaster GSS. Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi Genoscope.
Direct Submission AL069706.1 GI:4949849 (bases 1 to 1101) genomic survey sequence. /organism="Drosophila melanogaster" |mol type="genomic DNA" |db xref="taxon:7227" |clone="BACR29B23" /clone\_lib="RPCI-98" /note="end : T7" 4.8%; 34.8%; Score 97.8; DB 9; Pred. No. 8.7e-08; Length 1101; seqref@genoscope.cns.fr

Matches

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Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila please see http://www.fruitfly.org The BDGP Drosophila please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Mammoser in Pieter de Jong's laboratory in the Department (Cancer Genetics at the Roswell Park Cancer Institute in Buffallo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTCTGATTAGTCGATTACCGCCTTTTATAATTTTACAATACTGAGTAATATGAATAAAT 1557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCATAAGATTATAAAICTAIGTTATAATGATAATATAATTTTAAAAATAATACTATATTA 1497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATTAAATGGGACAGAGGGAGTAATACCTTTATGATATATAAATTTTTGTTATTTTGATT 1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WATWWTATWTWTTTWATWTATWTATTTATWTWTWTTWTATTWTATWTATATWWWTWWAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tamatatatamtaattumutwiatatwiamwwiatmatatatatuawittwiaaaatataww
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        genomic survey sequence.
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com Drosophila melanogaster /----
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       Mus musculus molossinus
Mus musculus molossinus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                         sequence.
AG386981
AG386981.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1059 DRWAWDDGAGTWWTATWWWWWWWWATWDTWWDKWWWWATAAKTDTAWTWWRTAWRADWAG 1000
                                                                                                                                                         Mus musculus molossinus
                                                                                                                                                                               AG386981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109;
                                                                                                                                                                                                                                                               TTWTTTAAWWWAAWWTATWAAWTAAAWAAAAAAAAAATTT
                                                                                                                                                                                                                                                                                              GTTTCAGAAATTTAAAATAATTATTGAGCATGGGAAGTT
                                                                                                                                                                                                                                                                                                                               TAAATCAGTTATCTGAAAAGCAAATAATATCTTTGTAAAACAGCGTTCGGTCAAATGGGA 1612
                                                                                                                                                                                                                                                                                                                                                        RTTÁRAÁNDWWÍWKAMDWÁKWDWKÍRÁDRWDRWAADTWTDARKADRDWAKARÁWRARRDR 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGADAGKGKKTGRKRRRDRATWDRTDAWWADAAWWTTTDTDTDDWDKRDRRRKGARRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATTAATTCTGATTAGTCGATTACCGCCTTTTATAATTTTACAATACTGAGTAATATGAA 1552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isogenic strain y2; cn bw sp, the same strain used for the BDC Pl and EST libraries. A more detailed description of the libra and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRWAADRTWDRDDDDDRDRAGTAGRKWRRTWKRRWKRRDTRWDDADADDTARDDRRRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGATTTCATAAGATTATAAATCTATGTTATAATGATAATATAATTTTAAAAATAATACTA 1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRDWGDRAGKRGGARKRRDRKRADDKRDAADDRDDAATWTTWTTTTRDTDDWKWKTDTW 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATAGAATTAAAIGGGACAGAGGGAGTAATACCTTTATGATATATAAATTTTTGTTATTT 1432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DWDWDKDWKWDGAKDRKADDDDGAGDKDDDGKGKDADDDTDGTKDDDDKDKMDDWDKAK
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                                                                                                       GI:47998186
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/clone_lib="RPCI-98"
/note="end : TET3"
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/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.7%;
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DNA,
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Pred. No. 1.1e-07;
1; Mismatches 210;
                                                                                                                                                bp DNA linear (
clone:MSMg01-201G10.TJ,
Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                  genomic survey
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REFERENCE AUTHORS TITLE

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RESULT 2 CNS0039G/c LOCUS DEFINITION

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abeertc.riken.jp). Tsukuba Institute, please contact Kuniya Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.Site 1
R.Site 2
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Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e-mail: abe@rtc.riken.jp
AAAACAAATTCAATGAGATAAAATATCTTACAATGAAAAGAAGGACAATGTCTCTTTGAA 1103
                                                                                                                                                                                                                                                                                                                       GTACAGGTTAAAACTTTTACAAGAATTTATATTAAACGAAAATCATTTATAACATGTCT
                                           АСТААGAAAAATGTATAAAGTAATGTAGAGTAAAAAGAAAGAGAAAGTGGGTAAA 1223
                                                                                                                                      ТАЛЛАТЛАЛАТАТААТЛАТАЛАЛАЛАТАТАЛАЛАЛАТАЛАЛАЛТАЛАЛАЛАЛА 684
                                                                                                                                                                              AAAACAAATAGGTACTCCCTCCGTCCCTCTGAAATGTATACATATGGATTGGACACGGAG
                                                                                                                                                                                                                            CTCGGCTGTCATTATAATAGGGATCACTTACTGATCATCCATTAA-----AACCTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                  ATAAGAGAGGTTAGTAAACAGAAAGCAGGTAAAAACAAGAGCTTGCTGCTGTGTTTAG 869
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/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue type="mixture of kidney and spleen"/clone_Tib="MSMg01 Mouse Male BAC Library"
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Pred. No. 2.2e-07;
0; Mismatches 523;
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                                                                                                                                                                                             Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BBGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by kazutoyo Osoegawa and melanogaster BAC library was prepared by kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's plant EST libraries. A more detailed description of the library
                                                                                                                              and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNS0039G 1101 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web : www.genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGTAAATTTAAATTAATTGTTATTTTTTGTTTCAGAAATTTAAAATAA 1692
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/db_xref="taxon:7227"
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    CL509408 1758 bp
SAIL_811_H11.v3 SAIL Collection
                                                                     WWWMHWWAHWATWW 1037
                                                                                          TAACATTCTAAATAT 2051
                                                                                                          CHMYHMMHMYMYCCHYYCTCHTHATTHYHYMCTCYHYCTWHTYWTAYMWAWTAHAMTTAT 1022
                                                                                                                              TCATCACATCAATCTTACACCACAAACCTTGAGCTTAATTTTTCTACTTATTCTCAGCAA 2036
                                                                                                                                                      ТНИСМСНЕНИН СТСНЕНН ТИХНИТ СНИМИНИНИНИНИНИМИА ТИМТ ТИТТИМИМС СМИНЕН
                                                                                                                                                                        TATCAACACCTCAACATTGATGTTAGCGTACTATAAATAGGTGCTCTTGGTGCTCTACTA 1976
                                                                                                                                                                                                 TWMHHTTTHWAWWHTHTWCWWWWHATTWTWATHCWACMTMHWHHMMHHHHMACHAHHH
                                                                                                                                                                                                           <u> ҮММҮҮММАҮҮММҮСТАСТҮНҮННННҮНМАҮНТТМҮАМАНАМММИННАНҮАААААМААМА</u>
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/note="end : TET3"
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na genomic clone
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Y Match 4.6%; Score 94.6; DB 9; Local Similarity 34.2%; Pred. No. 3.3e-07;
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Applied Trait Genetics
Syngenta Biotechnology Inc.
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
Bmail: allen.sessions@syngenta.com
ABRC Stock Number CS836276; T-DNA left border flanking sequences
Syngenta Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
Sessions, A., Burke, E., Presting, G., Aux, G., McElver, J., Pat Dietrich, B., Ho, P., Bacwaden, J., Ko, C., Clarke, J.D., Cotton Bullis, D., Snell, J., Miguel, T., Hutchison, D., Kimmerly, B., Mitzel, T., Katagiri, F., Glazebrook, J., Law, M. and Goff, S.A. A high-throughput Arabidopsis reverse genetics system Plant Cell 14 (12), 2985-2994 (2002)
                                             CTGCTGTGTGTTAGTTGTTGTGAGCTCATTTCTTTAAAAGTAATGTAAACTGATCTAAA 914
                                                                                           TTAAGTTACTAATAAATAAGAGAGGTTAGTAAACAGAAAGCAGGTAAAAACAAGAGCTTG
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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CL509408
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/clone="SAIL_811_H11.v3"
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/ecotype="Columbia"
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                              AACATTGATGTTAGCGTACTATAAAT 1954
                                                                                            ТССТТТТСТАРАСТТТТТАРАРТАРАРАРАНДИТЕТТАТТСТАРТТАТСЕРСТС 1928
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                                                              antaaataaataaanaatatataaaaaaaatataaatataaatataaaata
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Spemannstr. 37-39, Tuebingen
Tel: 00497071601371
Fax: 00497071601498
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Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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CG753083.1 GI:37977199
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P048-1-C01.za Ppa EcoRI BAC Library Pristionchus pacificus
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Evolutionary Biology
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 AAGAATTTATAATTAAACGAAAATCATTTTATAACATGTCTCTCGGCTGTCATTATAATAG
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                                                                                          AAAGCAGGTAAAAACAAGAGCTTGCTGCTGTGTGTTTAGTTGTTGAGCTCATTTCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest
the genomic DNA with EcoRI and cloning into the BAC
vector."
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"mol type="genomic DNA"

/strāin="California"

/db_xref="taxon:54126"
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    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 1202)

Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J., Warren,W., Graves,T., Mardis,E. and Wilson,R.

Gallus gallus BAC End Reads
Unpublished (2003)
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               942
                                                                                                                                                         Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata;
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Insert Length: 182000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
High quality sequence start: 30
High quality sequence stop: 105.
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/clone lib="CH261" | Site 1: EcoRI; Site 2: Eco CH261 | Female Chicken library - For library and clone ordering information: http://www.chori.org/bacpac"
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/strain="Red Jungle Fowl"
/db xref="texon:9031"
/clone="CH261-167M9"
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/mol_type="genomic DNA"
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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     TAGTACAGGTTAAAACTTTTACAAGAATTTATATTAAACGAAAATCATTTTATAACATGT
                                                                             CTCTCGGCTGTCATTATAATAGGGATCACTTACTGATCATCCATTAAAAACCTTGTTAAAA 1047
                                                                                                                                                         AGTTGTTGTGAGCTCATTTCTTTAAAAGTAATGTAAACTGATCTAAAGCACATAGAAATT 927
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/db_xref="taxon:7227"
/clone="BACR05N11"
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/mol_type="genomic DNA"
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/note="end : TET3"
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Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part collaboration with the Berkeley Drosophila Genome Project (BDG)
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department
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BACR29B23 of RPCI-98 library from Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                        AAAWTGKGAATGKKKKGKTARKKKGRKGTTAARAATDGTAAGAKRATAAKKTKTKAATKK
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AL069706.1 AL069706.1 GSS. Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi Eukaryota; Metazoā; Arthropoda; Hexapoda; Insecta; Pterygo Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. Drosophila melanogaster (fruit Drosophila melanogaster (bases 1 to 1101) fly) Pterygota;

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CL118721.1 GI:40612356
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       Xenopus tropicalis
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ilarity 34.7%;
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/mol_type="genomic DNA"
/db xref="taxon:7727"
/clone="BACR29B23"
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SOURCE

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Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTCACTATAGGG
Class: BAC ends
GAAAGTTTTGAAATGTATAGAATTGAGTGGGACATCCATAAAAGGAAAGTGTATAGAATT 1381
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1 (Dases I to 1608)

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.

A physical map of the xenopus tropicalis genome
                                                                        Similarity
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Contact: Richard K Wilson
                                      АТВАВАВАВАТВАВАВТВАВАВАТТВАВАВАВАТАТВТВЕТАВАВАТВАВАВАТВАВАВА
                                                                                                                                                          AAGAGAAAGAAAAGTGGGTAAAGTAGCGGGACCCACCAATATATAATTGATAGATTTAGA 1261
                                                                                                                                                                                                     TACATATGGATTGGACACGGAGACTAAGAAAATGTATAAAGTAATGTAGAGTAAAAAGA 1201
                                                                                                                                                                                                                                                                                                                      AGAAGGACAATGTCTCTTTGAAAAAACAAATAGGTACTCCCCTCCGTCCCTCTGAAATGTA 1141
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                                                                                                                                                                                                                                                                                    ТАЛЛАЛДАЛАТАТАЛДАТТТАЛАЛДАЛДАЛДАЛДАЛДАЛДАЛДАЛДА.--ЛАДДАЛДАЛДА
                                                                                                                                                                                                                                                                                                                                                                                               GATCATCCATTAAAACCTTGTTAAAACAAATTCAATGAGATAAAATATCTTACAATGAAA 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAAACGAAAATCATTTTATAACATGTCTCTCGGCTGTCATTATAATAGGGATCACTTACT 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTTGCTGCTGTGTTTAGTTGTTGTGAGCTCATTTCTTTAAAAGTAATGTAAAC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----TGATCTAAAGCACATAGAAATTTAGTACAGGTTAAAACTTTTACAAGAATTTATAT 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u> АТАРАТТАРАЛТАТРАЙАРАВААТБАРАРАВАТАЙАРАТАЙАРАВАТАТАТАЙАРАДАРА</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="ISB1"
/note="Vector: pBeloBAC11;
Library Segment 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/db_xref="taxon:8364"
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; Pred. No. 2e-00
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  996 АААЛЛЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАТАЛАЛАТТАЛАЛАТТАЛАЛТАЛАЛАЛАЛАЛАЛА
                                                                                                                                                                                                                                                                                                         National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jamie Thompson, University of WI
cDNA Library Preparation: Gina Zastrow-Hayes
cDNA Library Preparation: Gina Zastrow-Hayes
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (Linl)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1067)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1067 bp mRNA linear EST 30-WAY-2003
AGENCOURT 14286445 NIH_MGC_173 Homo sapiens cDNA 5', mRNA sequence.
CD386564
                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
plate: NDKW74 row: e column: 02
High quality sequence start: 8
High quality sequence stop: 462.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Daniela S. Gerhard,
Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo
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                                                /clone_lib="NIH_MGC_173"
/note="Vector: pDONR201, Site_1: attP2; Site_2:
/IDER_PRIMING - oligo dT; METHÖD - full-length er
// LIBR_PROVIDER - Bradfield"
                                                                                                                           /tissue_type="embryonic trophoblasts,
cells"
                                                                                                           'lab_host="DH10B TonA"
                                                                                                                                                                                     organism="Homo sapiens"
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                                                                                                                                                           xref="taxon:9606"
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   Score
    88.8;
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                                                                                                                                                                                                    sequence.
AG347098
AG347098.1
GSS.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
                                                                                           Hattori,M., Toyoda,A., Noguchi,H., BAC end Sequences of Library MSMg01
                                                                                                                                                                        Mus
                                                                                                                                                                                     Mue
                                                                                                                                                                                                                                                                  Mus musculus molossinus
                                              Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
                                                                           Unpublished
                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                 AG347098
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tive 0; Mismatches 376;
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DNA,
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                                                                                                                                                                                                                                                               bp DNA linear
clone:MSMg01-142102.T7,
                                                                                                           Kojima, T.
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genomic survey
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        1624 ATTCAATAGTTTTAATATAAAAGTAAATTTTAAATTTAATTGTTATTTTTGTTTCAGAAAT 1683
                                                                      1567 GAAAAGCAAAT----AATATCTTTGTAAAACAGCGTTCGGTCAAATGGGAAGTTCATGTGT
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R.Site 2
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Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken Tsukuba Institude, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
                                                                                                                                                                                                    TATAAATCTATGTTATAATGATAATATATTTTAAAAATAATACTATATTAATTCTGATT 1506
                                                                                                                                                                                                                                                            GGACAGAGGGAGTAATACCTTTATGATATATAAATTTTTGTTATTTTGATTTCATAAGAT 1446
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Similarity 45.58;
                                       AĀĀĀTAATĀĀTTAAĀTAĀTĀTĀTĀTĀTĀĀĀĀĀAAANTAATĀĀĀĀAAATĀĀTĪĀĀĀAATĀ 616
                                                                                                       AGTCGATTACCGCCTTTTATAATTTTACAATACTGAGTAATATGAATAAATCAGTTATCT 1566
                                                                                                                                                                      Sequencing : T7
LIBRARY
                                                                                                                                                                                                                                                                                                  TTTTGAAATGTATAGAATTGAGTGGGACATCCATAAAAGGAAAGTGTATAGAATTAAATG 1386
                                                                                                                                                                                                                                                                                                                                                                  AGTIGAAAGTAGTGGGIGGGATTTTTTATATTATAAAAATTTACTATTTTGAGAAAG 1326
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/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="MSMg01-142I02.T7"
/sex="male"
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                                                                                                                                                                                                                                                  Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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An integrated physical and genetic map of the nematode Pristionchu
                                                                                                                                                                                                                                             Fax: 00497071601498
                                                                                                                                                                                                                                                                                                                            Contact: Sommer RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 1392)
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                                                                                                                                                                                                                      ralf.sommer@tuebingen.mpg
                                                     /db_xref="taxon:54126"
/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest the genomic DNA with EcoRI and cloning into the BAC
                                                                                                                          /organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
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                                                                                                     GAAAGTGTATAGAATTAAATGGGACAGAGGGAGTAATACCTTTATGATATATAAATTTTT
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                                                                                                      41
                                                                                                                                                                                                                                                                                                                                                                                                                                                   I (bases 1 to 1277)
Kremitzki,C., Higginbotham,J., Warren,W., Graves,T., Mardis,E.
Gallus gallus BAC End Reads
Unpublished (2003)
Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                                                                                              Seq primer: RM1 TACGACTCACTATAGGGAGA
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CH261-180N11_RM1.1 CH261 Gallus
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Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                      Insert Length: 182000
                                                                                                                                                                                                                                                                                                                                                                                                       Email: submissions@watson.wustl.edu
Insert Length: 182000 Std Error: 0.00
               TATTTTAAACAATTTTTTTGAAATAAATAAAAAAAATAAAATAACATAAAATATTATT
                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                 /clone="CH261-180N11"
/sex="female"
                                                                                                                                                                                                                                                                                       /organism="Gallus gallus"
/mol_type="genomic DNA"
/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                             4.3%;
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Pred. No. 5.4e-06;
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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/clone_lib="CH261"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CH261 Female_Chicken library - for library and clone ordering information: http://www.chori.org/bacpac"
                                                                                                                                                                                                                                                   0; Mismatches 600;
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  and Wilson,R.
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Sakaki, Y.

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                             GI:47920150
                                                                    1696 bp DNA linear DNA, clone:MSMg01-142C12.T7,
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Li Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9171), Fax:81-45-503-9170, Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan Phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                                             775 АТТААЛАТТАGAGCTATTAATTAAGTTACTAATAAATAAGAGAGGTTAGTAAACAGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            464;
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                             ACTTACTGATCATCCATTAAAACCTTGTTAAAACAAATTCAATGAGATAAAATATCTTAC 1074
                                                                                                                              ATCATATTAAAATAATATCTATCAATAATAAACNTACAAACATAATATAAATATCACC
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                                                                                                                                                                                             CAGGTAAAAACAAGAGCTTGCTGCTGTGTTTAGTTGTTGTGAGCTCATTTCTTTAAAA 894
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Similarity 47.3%;
                                                               ATAAATAATAAAAAAATAAAAATAATAATAAAATCTTACTAAAATAAAAATATT--
                                                                                                                                                                                                                             GTAATGTAAACTGATCTAAAGCACATAGAAATTTAGTACAGGTTAAAAACTTTTACAAGAA 954
                                                                                                                                                                                                                                                              АТАЙАЙТАЙАСАААЙСАЙСАТЙЙТАТЙСАЙТАЙЛТАЙТАЙТАЙТАЙТАЙТАЙТАЙАЙДАЙСАЙЙАЙЙЙД 1171
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Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hattori,M., Toyoda,A., Noguchi,H., Kojima,T.
BAC end Sequences of Library MSMg01
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/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-142C12.T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue_type="mixture of kidney and spleen"
|clone_lib="MSMg01 Mouse Male BAC Library"
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Published Applications NA:*

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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Sequence 1, Appli Sequence 113786,	Sequence 490, App	GENERAL INFORMATI Sequence 6854, Ap	Sequence 240, App	Sequence 386, App	Sequence 1, Appli	Description

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US-10-027-632-113788 US-10-027-632-113788 US-10-027-632-113788 US-10-221-632-113788 US-10-221-632-113788 US-10-221-632-120 US-10-741-601-5746 US-10-311-445-191 US-10-311-455-191 US-10-240-453-107 US-10-311-455-1984 US-10-311-455-1984 US-10-311-455-1984 US-10-311-455-1984 US-10-311-455-1984 US-10-311-455-1984 US-10-311-455-1128 US-10-27-632-97533 US-10-27-632-11234 US-10-278-698-769 US-10-278-632-113786 US-10-278-632-113786

## ALIGNMENTS

Query Best 1 Matche	; TYP; ; ORG; ; FEA; ; OTH; US-10-4;	Seque Publi GENERA APPLI TITLI TITLI FILE CURRI CURRI NUMBI SEQ II	RESULT 1
atch cal 62	NISM: Artificial Sequence UTRE: R INFORMATION: chemically treated genomic DNA (Homo sapiens) 3-126-386	ice 386, Application US/10473126 ation No. US20040234973A1  LINFORMATION: LINFORMATION: CANT: Epigenomics AG CANT: Epigenomics AG OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell OF INVENTION: proliferative disorders REFERENCE: REFERENCE: NT APPLICATION NUMBER: US/10/473,126 NT FILING DATE: 2003-09-26 R OF SEQ ID NOS: 1258 NO 386	RESULT 1 US-10-473-126-386
	<pre>8%; Score 99.4; DB 18; Length 8056; 5%; Pred. No. 1.1e-07; 0; Mismatches 761; Indels 18; Gaps TTTTTATATGTAAAATAATGCCCATCCAAGGATAAGTAAAATTC 60</pre>	TYPE: DNA ORGANISM: Artificial Sequence PEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) -10-473-126-386 10-473-126-386 4.8%; Score 99.4; DB 18; Length 8056; Best Local Similarity 44.5%; Pred. No. 1.1e-07; Matches 624; Conservative 0; Mismatches 761; Indels 18; Gaps 548 ATGCTTCTCAAAATGTTTTTTATATGTTAAAATATGCCCATCCAAGGATAAGTAAAATTC 60	Sequence 386, Application US/10473126 publication No. US20040234973A1 SENERAL INFORMATION: APPLICANT: Epigenomics AG TITLE OF INVENTION: Methods and nucleic acids for the analysis of TITLE OF INVENTION: proliferative disorders FILE REFERENCE: CURRENT APPLICATION NUMBER: US/10/473,126 CURRENT FILING DATE: 2003-09-26 CURRENT FILING DATE: 2003-09-26 NUMBER OF SEQ ID NOS: 1258 SEQ ID NO 386 LENGTH: 8056 TYPE: DNA ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) -10-473-126-386 Duery Match Sept Local Similarity 44.5%; Pred. No. 1.1e-07; Matches 624; Conservative 0; Mismatches 761; Indels 18; Conservative 0; Misma

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US-10-312-841-1/c
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TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des 1
FILE REFERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
LENGTH: 3673778
TYPE: DNA
ORGANISN: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
FEATURE:
FEATURE:
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Best Local Similarity 43.8%;
Matches 587; Conservative
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Publication No. US20030186277A1
GENERAL INFORMATION:
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LOCATION: (3294164)
                             1714246 АТАПАДАДТАТАЛАДАТАТАТАТАЛАДАТАТАТАТАЛАДАТАТАТАДАДАТАТАТАЛАД
                                                                                                                                                1714365 ААААТАТАТАТАТАЛАЛАТАТАТАТАЛАЛАТАТАЛААНТАТАЛАТАТАЛАДАТАТАТАЛА 1714306
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                                                        GTCTCTCGGCTGTCATTATAATAGGGATCACTTACTGATCATCCATTAAAACCTTGTTAA 1045
                                                                                                                TTTAGTACAGGTTAAAACTTTTACAAGAATTTATATTAAACGAAAATCATTTTATAACAT 985
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RESULT 3
US-10-473-126-240
US-10-473-126-240
Sequence 240, Application US/10473126
Publication No. US20040234973A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
ITITLE OF INVENTION: Methods and nucleic acids for ITITLE OF INVENTION: proliferative disorders
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
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Best Local Simi
Matches 627;
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TYPE: DNA

ORGANISM: Artificial S
FEATURE:
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RESULT 4
US-10-473-126-386/c
US-10-473-126-386/c
Sequence 386, Application US/10473126
Publication No. US20040234973A1
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids
TITLE OF INVENTION: proliferative disorders
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CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 386
ENGIH: 8056
ENGIH: 8056
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA
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          AAAGCACATAGAAATTTAGTACAGGTTAAAACTTTTACAAGAATTTATATTTAAACGAAAA 971
                                                 ТААГТААСТТАСТААТАААТААGAGAGGGTTAGTAAACAGAAAGCAGGTAAAAACAAGAGC
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                                                                                                                                                                                                           Score 91.6; DE Pred. No. 2.6e-0; Mismatches
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                                    RESULT 5
US-10-473-126-240/c
Sequence 240, Application US/10473126
Publication No. US20040234973A1
GENERAL INFORMATION:
APPLICANT: EBJGENOMICS AG
TITLE OF INVENTION: Methods and nucleic acidity.
TITLE OF INVENTION: proliferative disorders.
FILE REPERSINCE:
CURRENT APPLICATION NUMBER: US/10/473,126
NUMBER OF SEQ ID NO 240
SEQ ID NO 240
LENGTH: 8056
TYPE: DNA
ORGANITOM: NO.
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FEATURE: OTHER INFORMATION: chemically treated genomic
                              ORGANISM: Artificial
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Matches 442; Conserv
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TTAAAAAAAATAA 427
                                                                                                       TCGATTACCGCCTTTTATAA-----TTTTACAATACTGAGTAATATGAATAAATCAGTTA 156:
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              TTAAAATAAATTA 1696
                              ACACGGAGACTAAGAAAAATGTATAAAGTAATGTAGAGTAAAAAAGAAAAGAAAAGAAAAG
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Pred. No. 9e-06;
0; Mismatches 519;
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GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF PHO
FILE REFERENCE: PTS-0011
CURRENT APPLICATION NUMBER: US/10/211,179
CURRENT FILING DATE: 2002-08-01
NUMBER OF SEQ ID NOS: 119
OTHER INFORMATION: n = a, t, c, or 9
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Best Local Similarity 46.0%;
Matches 458; Conservative
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ATAATACTATATTAATTCTGATTAGTCGATTACCGCCTTTTATAATTTTTACAATACTGAG 1543
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                                                                                           Score 83; DB 17; Length 158001; Pred. No. 0.00025; 0; Mismatches 530; Indels 7;
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Sequence 6854, Application US/1071993

Publication No. US20040265849A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASS
TITLE OF INVENTION: ALZHBIMER'S DISEASE, MET
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6854
LENGUTH: 74665
TYPE: DNA
ORGANISM: Homo sapiens
US-10-719-993-6854
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Best Local Similarity 44.8%;
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APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
TITLE OF INVENTION: Transcription
ITILE OF INVENTION: With DNA TRANScription
ITILE OF INVENTION: With DNA TRANScription
CURRENT APPLICATION NUMBER: US/10/240,453
PRIOR APPLICATION NUMBER: DO2-10-02
PRIOR APPLICATION NUMBER: PCT/EP01/03973
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
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                                                                                                                                                                                                                                  Sequence 206, Application US/10240453
Publication No. US20030148326A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OP SEQ ID NOS: 350
SEQ ID NO 206
LENGTH: 11745
TYPE: DNA
ATTIFICIAL Sequence
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Best Local Sin
Matches 499;
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NAME/KEY: unsure
LOCATION: (9105)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial FEATURE:
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                                                                                                                                          ATAACATAAAAAAAAACCTTTCAAAACAATAAAAATA--ATCAATTATCATATACT 4331
                                                                                                                                                                                                                                                               GTAGAGTAAAAAGAAAGAAAAGAAAAGTGGGTAAAGTAGCGGGACCCACCAATATATAA
                                                                                                                                                                                                                                                                                         CCCTCTGAAATGTATACATATGGATTGGACACGGAGACTAAGAAAAATGTATAAAGTAAT 1187
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                     TACTATATTAATTCTGATTAGTCGATTACCGCCTTTATAATTTTACAATACTGAGTAAT
                                              TATTTTGATTTCATAAGATTATAAATCTATGTTATAATGATAATAATTTTTAAAAATAA 1487
                                                                                             АТТАЛАЛАЛАТАЛАЛАТАЛТАЛАТАЛАЛАСАЛСАЛАТАТАЛАСЛАСТАТТАТАЛАЛАЛ 4151
                                                                                                                    AAGTGTATAGAATTAAATGGGACAGAGGGAGTAATACCTTTATGATATATAAAATTTTTGT
                                                                                                                                                                                          TTTÄAÄTCCTAÄAAACÄAAACTAAÄÄATCÄTTTAATTTATCAÄTÄTÄTÄACTCÄATÄÄT 4271
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Pred. No. 0.0027;
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TITLE OF INVENTION: Cytosine methylation
FILL REFERENCE: 5013.1014
CURRENT APPLICATION UNMER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION UNMER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION UNMER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER: OF SEQ ID NOS: 2424
SEQ ID NO 490
LEGITH: 5930
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION. Chamically treated denom-
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; Sequence 490, Application US/10311455
; Publication No. US20030143606A1
                                                                                                                                                              ; OTHER INFORMATION: chemically treated genomic DNA US-10-311-455-490
                                                                              Matches 371;
                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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AATTAAAAAAAAAAAAATAATATAAAAACATTTACTACTTTAAATATTTATAAACAAT 5095
                                    AATGTAAACTGATCTAAAGCACATAGAAATTTAGTACAGGTTAAAACTTTTACAAGAATT
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                                                                                Conservative
                                                                                                 3.5%;
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                                                                                0;
                                                                            Score 71; DB 15; I
Pred. No. 0.011;
0; Mismatches 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Associated with the Immune System by
                                                                                                                    Length 5930;
                                                                                                                                                                                    (Homo sapiens)
                                                                                  Indels
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CTAATTTATAATATTTCAAAACAATATTAAAATAAAACAAAAATACAAAATTAAATAAAA

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TTACTGATCATCATTAAAACCTTGTTAAAACAAATTCAATGAGATAAAATATCTTACAA 1076

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US-10-312-841-1
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                           Query Match
Best Local Similarity
Matches 644; Conserv
                                                                                                                   APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des
FILB REFERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
LENGTH: 3673778
TYPE: DNA
ORGANISM: Artificial Sequence
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Publication No. US20030186277A1
GENERAL INFORMATION:
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                                                                             NAME/KEY: unsure
LOCATION: (3294164)
                                                                                                          FEATURE:
OTHER INFORMATION:
                                                                                                  FEATURE:
1435
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                                                                                                                                                                                                                                                                                                     TTCAAAAATTTAATTCAAA 4362
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ilarity 42.2%;
Conservative
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                      Score 70.6; DB 16;
Pred. No. 0.12;
0; Mismatches 874;
                      Indels
                                          Length
                                        3673778;
                     9;
                     Gaps
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1714693 TATATGTATATTTTATATGTATATTTTATATGTATATTTTATATGTATATTTTATATATATA
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1225 TAGCGGGACCCACCATATATATTGATAGATTTAGAAAAGTAGTTGAAAGTAGTGGGTG 1284
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                                                                                                                           TATTTTÄTATATATATTTTTATATATATATTTTATÄTÄTÄTTTTTATATATATÄTÄTTTTTGT
                                                                                                                                                         AAACAAATAGGTACTCCCTCCGTCCCTCTGAAATGTATACATATGGATTGGACACGGAGA
                                                                                                                                                                                            ATATATTATATTTTATATATATATAGTATATATATTTTATATGTATATATTTTATATA
                                                                                                                                                                                                                              AAACAAATTCAATGAGATAAAATATCTTACAATGAAAAGAAGGACAATGTCTCTTTGAAA 1104
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-12
PRIOR PELLING DATE: 2000-04-20
PRIOR PELLING DATE: 2000-04-20
PRIOR PELLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PELLING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PELLING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOPTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 113786
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US-10-027-632-113786/c
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                                                                                                         Matches 474;
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108027.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                TYPE: DNA
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                                                                                                                    Match 3.4%;
Local Similarity 43.6%;
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 681
 GACTTAGGTCAAAAATGGACGCTGGTAAACAGCCTAGACTTGGTCACTGATAAATAGATA 740
                                   TTAATACTAACAATTTTTATACTTATATTAATGAGTTTAATATGTTTATACTGTAATATA
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                                                                    TTGTTAATATATATGTTTACACTTACAAGAGGATATTCGTAATACTTTTAGACGACAAGA 680
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                                                                                                         Conservative
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                                                                                      AAATAAAT 1694
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                                                                                                                                                                                                                              GAAAAGCAAATAATCTTTGTAAAACAGCGTTCGGTCAAATGGGAAGTTCATGTGTATT
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CURRENT FAPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-04-20

PRIOR PRILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/165,218

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR PRILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR PRILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR PILLING DATE: 1999-09-28

PRIOR PILLING DATE: 1999-09-28

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; ORGANISM: Human
US-10-027-632-113787
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; Sequence 113787, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
GENERAL INFORMATION: David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
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Best Local Similarity 43.6
274, Conservative
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SOFTWARE: FastSEQ for Windows Version
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                                CCATTAAAACCTTGTTAAAACAAATTCAATGAGATAAAATATCTTACAATGAAAAGAAGG 1087
                                                                                                                                                                 AAAATCATTTTATAACATGTCTCTCGGCTGTCATTATAATAGGGATCACTTACTGATCAT
                                                                ACAATGTCTCTTTGAAAAAACAAATAGGTACTCCCTCCGTCCCTCTGAAATGTATACATA 1147
                                                                                                                                                                                                                                    TCTGGTTAÁCTATTÁTATATAGTTAÁCCATÁTTAÁAATATÁTAÁAATÁTATÁAÁTAÁTAÁTÁCA 1955
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                                                                                                                                                                                                                                                                                                     AGCTTGCTGCTGTGTTTAGTTGTTGTGAGCTCATTTCTTTAAAAGTAATGTAAACTGA 908
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Pred. No. 0.014;
0; Mismatches 600; Indels 1
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US-10-027-632-113788/c
; Sequence 113788, Application US/10027632
; Publication No. US20020198371A1
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       ORGANISM: Human
-10-027-632-113788
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SOFTWARE: FastSEQ for
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                              ENGTH:
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Query Match
Best Local Similarity
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CAATAGTTTTAATATAAAAGTAAATTTTAAATTAATTGTTATTTTTGTTTCAGAAATTTA 1686
                                          ттататаататататататтаттСатататттатататтттаатататGTTTAACTATA 1295
                                                                                                                                 AGTCGATTACCGCCTTTTATAATTTTTACAATACTGAGTAATATGAATAAATCAGTTATCT
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                                                                                     GAAAAGCAAATAATATCTTTGTAAAACAGCGTTCGGTCAAATGGGAAGTTCATGTGTATT 1626
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Pred. No. 0.014;
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/167,363
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US-10-027-632-113786/c
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Best Local S
Matches 474
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 113786
LENGTH: 3252
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Publication No. US20030204075A9
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Local Similarity 43.6%;
Les 474; Conservative
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                       AAAATCATTTTATAACATGTCTCTCGGCTGTCATTATAATAGGGATCACTTACTGATCAT 1027
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RESULT 15

US-10-027-632-113787/c

Sequence 113787, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827,129

CURRENT PILLING DATE: 2002-04-30

PRIOR PILLING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILLING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,5218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,363

PRIOR APPLICATION NUMBER: US 60/185,363

PRIOR FILLING DATE: 1090-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILLING DATE: 1999-11-23

PRIOR FILLING DATE: 1999-11-23

PRIOR FILLING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILLING DATE: 1999-09-28

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NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PastSEQ for Windows Version
SEQ ID NO 113787
LENGTH: 3252
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Search completed: March 15, 2005, 18:25:12 Job time : 1198.48 secs	1234 CAGTAAGT 1227	1687 AAATAAAT 1694	1294 TATAATAGTTAGCATATTAATAAGTTAATTTACTATATTAATTTAATTTAATATAAAGTTAA 1235	1627 CAATAGTTTTAATATAAAAGTAAATTTAAATTAATTTATTTTTT	1354 TTATATATATATATATATATTATTCATATATTTATATATTTTAATATGTTTAACTATA 1295	1567 GAAAAGCAAATAATATCTTTGTAAAACAGCGTTCGGTCAAATGGGAAGTTCATGTGTATT 1626	1414 TATTATGTAATTGATTTTATTATTATGTTAATATAATGTAATGCAAATTATATATA	1507 AGTCGATTACCGCCTTTTATAATTTTTACAATACTGAGTAATATGAATAAATCAGTTATCT 1566

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1: /cgn2_6/ptodata/1/pna/PCTUS1_COMB.seq:*

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46. / cgm2 6/ptcodate///pna/US099F COMB. seq; *
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67. / cgm2 6/ptcodate///pna/US101DA_COMB. seq; *
68. / cgm2 6/ptcodate///pna/US101DA_COMB. seq; *
69. / cgm2 6/ptcodate///pna/US101DA_COMB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                            Sequence 1, Appli Sequence 7, Appli Sequence 7, Appli Sequence 3, Appli Sequence 4, Appli Sequence 2, Appli Sequence 1, Appli Sequence 386, App Sequence 240, Appli Sequence 240, Appli Sequence 240, Appli Sequence 461, Appli Sequence 461, App Sequence 461, App Sequence 643, App Sequence 51800, A Sequence 15940, A Sequence 294, App Sequence 15940, A Sequence 16551, A Sequence 16551, A Sequence 179, App Sequence 2442, Appl Sequence 2442, Appl Sequence 27, Appl Sequence 24327, A 
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GENERAL INFORMATION:
APPLICANT: NISHIKAWA, SATOMI
APPLICANT: OEDA, KENJI
TITLE OF INVENTION: PLANT PROMOTERS AND PLANT TERMINATORS
FILE REFERENCE: 7372-70911
CURRENT APPLICATION UNMEER: US/09/806,197
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 2052
TYPE: DNA
ORGANISM: Daucus carota
US-09-806-197-1
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                   TGGTCACTGATAAATAGATAATTGTTAGTATAATATAGTAGGATCTACAATGACATTAAA
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Sequence 7, Application US/09806197
GENERAL INFORMATION:
APPLICANT: NISHIKAWA, SATOMI
APPLICANT: OEDA, KENJI
TITLE OF INVENTION: PLANT PROMOTERS AND PLANT TER
FILE REFERENCE: 7372-70911
CURRENT APPLICATION NUMBER: US/09/806,197
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 2052
TYPE: DNA
ORGANISM: Daucus carota
US-09-806-197-7
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US-09-806-197-5
; Sequence 5, Application US/09806197
; Sequence 5, Application US/09806197
; GENERAL INFORMATION;
APPLICANT: NISHIKAWA, SATOMI
; APPLICANT: OEDA, KENNI
; TITLE OF INVENTION: PLANT PROMOTERS AND PLANT TERMINATORS
; FILE REFERENCE: 7372-70911
; CURRENT APPLICATION NUMBER: US/09/806,197
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PATENTIN Ver. 2.1
; SEQ ID NO 5
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; TYPE: DNA
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                                               TCTCATTTCTACTCCACTTCTTTGCTATAAGCAAGAAATCACTTCTTTTAAGCTAACCCA 240
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Sequence 3, Application US/09806197
GENERAL INFORMATION:
APPLICANT: NISHIKAMA, SATOMI
APPLICANT: OEDA, KENJI
TITLE OF INVENTION: PLANT PROMOTERS AND PLANT TEI
FILE REFERENCE: 7372-70911
CURRENT APPLICATION NUMBER: US/09/806,197
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3.4
ery Match 99.0%; Score 2030.8; st Local Similarity 99.7%; Pred. No. 0; tches 2046; Conservative 0; Mismatches
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9-806-197-3
                                                  TYPE: DNA
ORGANISM: Daucus
9-806-197-3
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RESULT 5 US-09-806-197-4 ; Sequence 4, Application US/09806197 ; GENERAL INFORMATION: ; APPLICANT: NISHIKAWA, SATOMI	1951 CACATCARTCTTACACCACAAACCTTGAGCTTAATTTCTACTATTCTCAGCAATAAC 2040	AACACCTCAACATTGATGTTAGCGTACTATAAATAGGTGCTCTTGGTGCTCTACTATCAT		AACAATGTATGTCCGGTGTACATCTATGACCTTTCAACTCAAACTAGTGAATAAT 	1681 AATTTAAAATAAATTATTGAGCATGGGAAGTTCACGGGCATCATTGAGCAGCACTAGACT 1740 		TTATCTGAAAAGCAAATAATATCTTTGTAAAACAGCGTTCGGTCAAATGGGAAGTTCATG	1501 CTGATTAGTCGATTACCGCCTTTTATAATTTTACAATACTGAGTAATATGAATAAATCAG 1560	1441 TAAGATTATAAATCTATGTTATAATGATAATATATTATAAAAATAATAATATTAATT 1500 	1381 TAAATGGGACAGAGGGAGTAATACCTTTATGATATATATA	1321 AGAAAGTTTTGAAATGTATAGAATTGAGTGGGACATCCATAAAAGGAAAGTGTATAGAAT 1380 	1261 AAAAGTAGTIGAAAGTAGTGGGTGGGTGGGATTTTTATATTATAAAAATTTACTATTTTG 1320 	1201 AAAGAGAAAGAAAAGTGGGTAAAGTAGCGGGACCCACCAATATATAATTGATAGATTTAG 1260 	1141 ATACATATGGATTGGACACGGAGACTAAGAAAATGTATAAAGTAATGTAGAGTAAAAAG 1200	1077 AAGAAGGACAATGTCTTTGAAAAAACAAATAGGTACTCCCTCC

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; APPLICANT: OEDA, KENJI
; TITLE OF INVENTION: PLANT PROMOTERS AND PLANT TERMINATORS
; FILE REFERENCE: 7372-70911
; CURRENT APPLICATION UNUMER: US/09/806,197
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PATENTIN VET. 2.1
; SEQ ID NO 4
; LENGTH: 2048
; TYPE: DNA
; ORGANISM: Daucus carota
US-09-806-197-4
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Best Local Similarity 99.7%;
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                                  GATTGGAATCCTTTTCTAAACTTTTTTAAAATAAAAAATGCATTATTGTAATATTTATC
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AACACCTCAACATTGATGTTAGCGTACTATAAATAGGTGCTCTTGGTGCTCTACTATCAT
                                                                       GTTTGAACAATGTATGTCCGGTGTACATCTATGACCTTTCAACTCAAACTAGTGAATAAT
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; LOCATION:
US-09-300-487-2
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US-09-300-487-2
                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                   Matches 367;
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GENERAL INFORMATION:
APPLICANT: TORIKAI, Satomi
APPLICANT: OEDA, Kenji
                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703)205-8050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Stewart, Raymond C.
REGISTRATION NUMBER: 21.066
REFERENCE/DOCKET NUMBER: 214
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)205-8000
                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DI
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/911,434 FILING DATE: 12-AUG-1997 ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy COMPUTER: IBM PC COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: PLANT PROMOTER AND UTILIZATION NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                     ORGANISM: Daucus ca
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                         LENGTH: 2042 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                            1610 GGAAGTTCATGTGTATTCAATAGTTTTAATATATAAAGTAAATTTTAAATTTAATTGTTATT
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    CCAAGTTCACGTGTATTCTAAAATGTTAATACTAACATGAGTATTTTCTT--TTCAAGGT
                                                             AAATTATTTATCTGAATGATAACATCTTTGTAAACAAAACTGGGCCAAATAGGACCATAA 1602
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FALLS CHURCH
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                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 base pairs
TYPE: nucleic acid
ORIGINAL SOURCE:
            MOLECULE TYPE: DI
HYPOTHETICAL: NO
                                                                                                                                          NAME: Stewart, Raymond C.
REGISTRATION NUMBER: 21,066
REFERENCE/DOCKET NUMBER: 21/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)205-8000
                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                           STRANDEDNESS:
TOPOLOGY: lir
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(703) 205-8050

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US 08/911,434

linear

DNA (genomic) single

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US-09-300-487-1
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 12-AUG-1997
                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                           MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: TORIKAI, Satomi
APPLICANT: OEDA, Kenji
TITLE OF INVENTION: PLANT
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
                                                                     APPLICATION NUMBER: FILING DATE:
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T: P.O. BOX 747
PALLS CHURCH:
VIRGINIA: VIRGINIA STATES OF AMERICA
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N: PLANT PROMOTER AND UTILIZATION THEREOF
                                                                                      US/09/300,487
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GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 386
LENGTH: 8056
TYPE: DNA
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Best Local Similarity 89.6%;
Matches 223; Conservative
                                                                                                                                                                                                                                            Matches 624;
                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo
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CTATTAATTAAGTTACTAATAAATAAGAGAGGTTAGTAAACAGAAAGCAGGTAAAAACAA
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                                                                                       ATGCTTCTCAAAATGTTTTTTATATGTAAAATAATGCCCATCCAAGGATAAGTAAAATTC 607
                                       TTAGACGACAAGACTTAGGTCAAAAATGGACGCTGGTAAACAGCCTAGACTTGGTCAC
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                                                              TGATAAATAGATAATTGTTAGTATAATATAGTAGGATCTACAATGACATTAAAATTAGAG
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ISOLATE: Kurc
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                                                                                                                                                                                                                                          4.8%; Score 99.4; DB 55;
44.5%; Pred. No. 1.2e-06;
ative 0; Mismatches 761;
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Pred. No. 1.8e-23;
0; Mismatches 24;
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APPLICANT: WANG, RONG-LIN

APPLICANT: WANG, RONG-LIN

ITILE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE

ITILE OF INVENTION: REPEAT MARKERS AND THEIR USES

FILE REFERENCE: NADII.058C1

CURRENT APPLICATION NUMBER: US/10/266,090

CURRENT APPLICATION NUMBER: US 10/260,703

PRIOR APPLICATION NUMBER: US 60,703

PRIOR FILING DATE: 2002-09-26

PRIOR FILING DATE: 2001-09-26

NUMBER OF SEQ ID NOS: 51812

SOFTWARE: FASTSEQ for Windows Version 4.0

LENGTH: 1069

TYPE: DNA

ORGANISM: HORDEUM VULGARE
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; NAME/KEY: misc_feature
; LOCATION: (1)...(1069)
; OTHER INFORMATION: n = A,T,C
US-10-266-090-13474
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Local Similarity 39.9%;
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Pred. No. 3.6e-06;
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CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 240
LENGTH: 8056
TYPE: DNA
TYPE: DNA
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TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
TITLE OF INVENTION: proliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 386
LENGTH: 8056
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Best Local Similarity
Matches 455; Conserv
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APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids
TITLE OF INVENTION: proliferative disorders
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ORGANISM: Artificial Sequence
FEATURE:
1507
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                                                                                           AGAGGGAGTAATACCTTTATGATATATATATATTTTTGTTATTTTTGATTTCATAAGATTATA 1450
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                          AATCTATGTTATAATGATAATATAATTTTAAAAATAATACT----ATATTAATTCTGATT
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Pred. No. 2.6e
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RESULT 13
US-10-473-126-240/c
; Sequence 240, Application US/10473126
; GENERAL INFORMATION:
, APPLICANT: Epigenomics AG
, TITLE OF INVENTION: Methods and nucleic acids for the analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver. 2
SEQ ID NO 2
LENGTH: 851
TYPE: DNA
ORGANISM: Daucus carota
US-09-806-197-2
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US-09-806-197-2/c
Sequence 2, Application US/09806197
GENERAL INFORMATION:
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APPLICANT: OEDA, KENJI
TITLE OF INVENTION: PLANT PROMOTERS AND PLANT
FILE REFERENCE: 7372-70911
CURRENT APPLICATION NUMBER: US/09/806,197
NUMBER OF SEQ ID NOS: 29
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Pred. No. 5.4e-05;
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-240
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Best Local
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SEQ ID NO 240
LENGTH: 8056
TYPE: DNA
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442;
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                                                                                                                     GGAGTAATACCTTTATGATATATAAATTTTTGTTAT-----TTTGATTTCATAAGATTA
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Pred. No. 8.3e-05;
0; Mismatches 519
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US-10-211-179-11
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Best Local Similarity
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CURRENT FILING DATE: 2002-08-01
NUMBER OF SEQ ID NOS: 119
OTHER INFORMATION: n = a, t, c, or g
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APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF
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                                                                                                                                                                                                                                                                                                                                                 TTTAAAAGTAATGTAAACTGATCTAAAGCACATAGA-AATTTAGTACAGGTTAAAACTTT
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                         AAATTTACTATTTTGAGAAAGTTTTGAAATGTATAGAATTGAGTGGGACATCCATAAAAG
                                                       ATGTAGAGTAAAAAAAAGAGAAAAGAAAAGTGGGTAAAGTAGCGGGACCCACCAATATAT 1245
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; ORGANISM: Human
; FEATURE:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(464387)
; OTHER INFORMATION: n = A,T,C or G
US-09-948-941-643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-09-948-941-643/c
Sequence 643, Application US/09948941
; GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH CANCER, METHODS OF DETECTION AND OF THE REFERENCE: CL000788
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 643
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Best Local Similarity 44.2%;
Matches 523; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/948,941
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/231,328
PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 464387
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                                                                                                                                                                                                                                                          732 AAATAGATAATTGTTAGTATAATATAGTAGGATCTACAATGACATTAAAATTAGAGCTAT 791
 AAAAATATATAAAATATATATATGTTATATATAAAATATAA ----TATGTTATATATAAT 359648
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                                                       AAAGCACATAGAAATTTAGTACAGGTTAAAACTTTTACAAGAATTTATATTAAACGAAAA 971
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Pred. No. 0.0028;
0; Mismatches 649;
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1152 359407 1212 359347 1272 359347 1272 359287 1332 359227 1391 359167 1451 359167 1451 359047 1511 359047 1684 1684 1744 1358867 1804 1804 1804 1804 1804 1804 1804 1804	ω <sub>2</sub>		
	10:	1032	;
		1032 TAAAACCTTGTTAAAACAAATTCAATGAGATAAAATATCTTACAATGAAAAGAAGGACAA 1091 	

Search completed: March 15, 2005, 17:31:32 Job time: 7607.94 secs

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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
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1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*

5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*

6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*

7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*

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9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
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Match
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Copyright (c) 1993 - 2005 Compugen Ltd.
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          US-60-655-875-31136

US-10-517-441-294

US-10-517-441-568

US-11-033-545-786

US-11-033-545-786

US-10-517-441-294

US-10-517-441-294

US-10-517-441-294

US-10-517-441-264

US-10-32-182A-166179

US-10-517-441-294

US-10-517-441-293

US-10-517-441-567

US-60-655-875-30892

US-60-655-875-31280

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Sequence 31136, A Sequence 568, App Sequence 568, App Sequence 293, App Sequence 567, App Sequence 568, App Sequence 568, App Sequence 568, App Sequence 564, App Sequence 564, App Sequence 564, App Sequence 290, App Sequence 291, App Sequence 293, App Sequence 293, App Sequence 293, App Sequence 293, App Sequence 567, App Sequence 567, App Sequence 510, App Sequence 51034, App Sequence 512, App
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2.8	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9
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Sequence 82000, A	Sequence 6143, Ap	Sequence 5707, Ap	Sequence 786, App	Sequence 592, App	Sequence 283, App	Sequence 23235, A	Sequence 679, App	Sequence 701, App	•	Sequence 543, App	Sequence 3822, Ap	Sequence 1, Appli	Sequence 1, Appli	Sequence 703, App	Sequence 59297, A	Sequence 578, App	Sequence 24622, A	Sequence 4, Appli	Sequence 557, App	occurre tootoo,

## ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR PLICATION NUMBER: DE 10317955.0
PRIOR PILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR APPLICATION NUMBER: DE 1030096.8
PRIOR FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779.4
                                                                                                                                                                                                        APPLICANT: FOEKENS, John
APPLICANT: HARBECK, Nadia
APPLICANT: MAIR, Sabine
APPLICANT MAIRR, Sabine
APPLICANT: MAIRR, Sabine
APPLICANT: MAIRR, Sabine
APPLICANT: MANGRICH, Inko
APPLICANT: RUJAN, Tamas
APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Manfred
APPLICANT: SCHMITT, Manfred
APPLICANT: LOOK, Maxime P
APPLICANT: MARX, Almuth
APPLICANT: MARX, Almuth
APPLICANT: HOEFLER, Heinz
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; OTHER INFORMATION: chemically treated US-10-517-441-294
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Best Local Similarity 44.6%;
Matches 358; Conservative (
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NUMBER OF SEQ ID NOS: 2147
SEQ ID NO 294
LENGTH: 5286
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ORGANISM: Artificial Sequence
FEATURE:
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 ATAAAATTATACTTTAAATTCT
                        TCAGAAATTTAAAATAAATTAT 1697
                                                TTATATTTATATATTATATATATATATCATATAAATATATATATATATATATATATATAT
                                                                       TCATGTGTATTCAATAGTTTTAATATAAAGTTAAATTTTAAATTTAATTGTTATTTTTGTT
                                                                                                    ATCAGTTATCTGAAAAAGCAAATAATATCTTTGTAAAACAGCGTTCGGTCAAATGGGAAGT 1615
                                                                                                                                                        TAATTCTGATTAGTCGATTACCGCCTTTTATAATTTTTACAATACTGAGTAATATGAATAA 1555
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Pred. No. 0.00017;
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APPLICANY: MARCA, CALINGE, APPLICANY: HOEFLER, Heinz
APPLICANY: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT APPLICATION NUMBER: DS/10/517,441
CURRENT APPLICATION NUMBER: ECT/EP2003/010881
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR FILING DATE: 2003-01-01
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10317956.8
PRIOR PILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR PILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR PILING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
SEQ ID NO 568
LENGTH: 5286
TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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Best Local S
Matches 358
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MODEL, Fabian
NIMMRICH, Inko
                                                                                            TTTAGAAAAGTAGTTGAAAGTAGTGGGTGGGTGTGGGATTTTTATATATAAAAATTTACTA 1315
                                                                                                                                                          AAAAGAAAGAGAAAAGAAAAGTGGGTAAAGTAGCGGGACCCACCAATATATAATTGATAGA 1255
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SCHMITT, Armin
SCHMITT, Manfred
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US-11-033-545-592

Sequence 592, Application US/11033545

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH INFLANDATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: C1000790

CURRENT APPLICATION NUMBER: US/11/033,545

CURRENT APPLICATION NUMBER: US/11/033,545

CURRENT FILING DATE: 2005-09-08

NUMBER OF SEQ ID NOS: 10823

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 592

LENGTH: 18651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.3%;
Best Local Similarity 48.8%;
Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Human
                                                                                                                                                 10123
                                                                                                                                                                                                                                                                                                                                                                                                       1201 AAAGAGAAAAGAAAAGTGGGTAAAGTAGCGGGACCCACCAATATATAAATTGATAGATTTAG 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4165
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                                                                       TATTAATTTAACTTAATTAATTAATTTAATATTAAATT--AAATTTTAATATTTTAAT 1023:
                                                                                                      TAAGATTATAAATCTATGTTATAATGATAATATATAATTTTAAAAATAATACTATATTAATT
                                                                                                                                                 TTAATATTA-----AATTAATTTAATTTAATATTAATTTAACTTAATTTAATTTAA
                                                                                                                                                                                  TAAATGGGACAGAGGGAGTAATACCTTTATGATATATAAATTTTTGTTATTTTGATTTCA 1440
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Pred. No. 0.00053;
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RESULT 5
US-11-033-545-786
; Sequence 786, Application US/11033545
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS:

TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOO0790
CURRENT APPLICATION NUMBER: US/11/033,545
CURRENT APPLICATION NUMBER: US/11/033,545
CURRENT FILING DATE: 2005-01-12
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FRACESEQ for Windows Version 4.0
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Best Local Similarity 48.8%;
Matches 250; Conservative
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                    AATTTAAAATAAATTATTGAGCATGGGAAGTT 1712
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                                                                                                                                                                                                      TTTAATTTÄÄTTTÄÄTATTAÄTTAATTTÄÄTTTTAATTTTAATTTAATTGCTTCAATATTAAATT
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APPLICANT: RUJAN, Tamas

APPLICANT: RUJAN, Tamas

APPLICANT: SCHMITT, Armin

APPLICANT: SCHMITT, Manfred

APPLICANT: LOOK, Maxime P.

APPLICANT: LOOK, Maxime P.

APPLICANT: MOSFLER, Heinz

ITILE OF INVENTION: Method and nucleic acids for ITILE OF INVENTION: MUMBER: US/10/517,441

CURRENT APPLICATION NUMBER: DCT/EP2003/010881

PRIOR APPLICATION NUMBER: DE 10317955.0

PRIOR FILING DATE: 2003-01-01

PRIOR APPLICATION NUMBER: DE 10300096.8

PRIOR APPLICATION NUMBER: DE 10300096.8

PRIOR APPLICATION NUMBER: DE 10245779.4

PRIOR FILING DATE: 2003-01-07

PRIOR FILING DATE: 2003-01-07

PRIOR APPLICATION NUMBER: DE 10245779.4

PRIOR FILING DATE: 2003-10-01

PRIOR FILING DATE: 2003-10-01

PRIOR FILING DATE: 2003-10-01

PRIOR FILING DATE: 2003-01-07

PRIOR PRIOR DATE: 2003-01-07

PRIOR PR
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US-10-517-441-293
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APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
APPLICANT: MAIER, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: chemically treated genomic DNA (Homo
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                            1098 TTTGAAAAAACAAATAGGTACTCCCTCCGTCCCTCTGAAATGTATACATATGGATTGGAC 1157
                                                                                                                                                                                                                                                                                                                                                                            1038 СТТСТТАЛАДСАЛАТТСАЛТСАСТАЛАЛАТАТСТТАСДАТСАЛДАДАДСАДСТАТСТС 1097
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GGTAAAGTAGCGGGACCCAACATATATAATTGATAGATTTAGAAAAGTAGTTGAAAGTA 1277
                                                                                                                                                           ATAGAAATTTAGTACAGGTTAAAACTTTTTACAAGAATTTATATTAAACGAAAATCATTTT 978
                                                                                                          TGTTTATTTÄGATTTTTTTTTTTTTATTTGTTGTGAATTTTGTATGTTATATATAT
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MODEL, Fabian
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Pred. No. 0.00074;
0; Mismatches 581
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cell

TYPE: DNA
ORGANISM: Human
-11-033-545-786

LENGTH: 18682

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RESULT 7
US-10-517-441-567
; Sequence 567, Applic; GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: method and nucleic acids for the improved treatment of breast
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR PILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR APPLICATION NUMBER: DE 10300096.8
                                                                                                                                                                                                                                                                          APPLICANT: FOEKENS, John
APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
APPLICANT: MAIER, Sabine
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MODEL, Fabian
NIMMRICH, Inko
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTCCGGTGTACATCTATGACCTTTCAACTCAAACTAGTGAATAATGCATTCTAGAATAC
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                                                                                                                                                                                       RUJAN, Tamas
SCHMITT, Armin
SCHMITT, Manfred
                                                                                                                                                           MARX, Almuth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR FILING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
SEQ ID NO 567
LENGTH: 5286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                         ATAATATCTTTGTAAAACAGCGTTCGGTCAAATGGGAAGTTCATGTGTATTCAATAGTTT 1635
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Conservative
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Pred. No. 0.00074;
0; Mismatches 581;
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CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR FILING DATE: 2003-04-17
PRIOR FILING DATE: 2003-04-17
PRIOR FILING DATE: 2003-04-17
PRIOR FILING DATE: 2003-04-17
PRIOR FILING DATE: 2003-01-07
PRIOR FILING DATE: 2003-01-07
PRIOR FILING DATE: 2003-01-07
PRIOR FILING DATE: 2002-10-01
PRIOR FILING DATE: 2002-10-01
PRIOR FILING DATE: 2002-10-01
SEQ ID NO 294
LENGTH: 5286
TYPE: NNA
                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                              Query Match 3.3%;
Best Local Similarity 44.7%;
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US-10-517-441-294
                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Manfred
APPLICANT: SCHMITT, Manfred
APPLICANT: LOOK, Maxime P.
APPLICANT: MARX, Almuth
APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
FILE REFERENCE: 47675-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 294, Application US/10517441
GENERAL INFORMATION:
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                                                                                                                                                                             895 GTAATGTAAACTGATCTAAAGCACATAGAAATTTAGTACAGGTTAAAACTTTTACA----
                                                                                                                                                   775 АТТАРАЛІТАGAGCTATTAATTAAGTTACTAATAAATAAGAGAGGTTAGTAAACAGAAAG 834
                                                                                                                                                                                                       715 TAGACTIGGICACIGATAAATAGATAAITGTTAGTATAATATAGTAGGATCTACAAIGAC 774
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                                                                 CAGGTAAAAACAAGAGCTTGCTGCTGTGTGTTTAGTTGTTGTGTGAGCTCATTTTCTTTAAAA 894
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NIMMRICH, Inko
RUJAN, Tamas
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KOENIG, Thomas
MAIER, Sabine
MARTENS, John
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                                                                                                                                                                                                                                            Score 67; DB 7;
Pred. No. 0.00088;
0; Mismatches 535
                                                                                                                                                                                                                                                                       Length 5286
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         Sequence 568, Application US/10517441
GENERAL INFORMATION:
APPLICANT: FORENS, John
APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
APPLICANT: KOENIG, Thomas
APPLICANT: MARIER, Sabine
APPLICANT: MARIER, Sabine
APPLICANT: MODEL, Fabian
APPLICANT: NUMRICH, Inko
APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Manfred
APPLICANT: SCHMITT, Manfred
APPLICANT: LOOK, Maxime P.
APPLICANT: HOEFLER, Heinz
APPLICANT: HOEFLER, Heinz
APPLICANT: HOEFLER, Heinz
APPLICANT: HOEFLER, Heinz
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                                                                                                                                                                                                                                                                                                                                              TTCGGTCAAATGGGAAGTTCATGTGTGTATTCAATAGTTTTAATATAAAAGTAAATTTTAAA 1657
                                                                                                                                                                                                                                                                                                                                                                                                                               АСТБАБТАЛТАТБАЛТБАЛТСАБТТАТСТБААЛАБСАЛАТАЛТАТСТТТБТАЛАДСАБСБ 1597
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAATTITTGTTATTTTGATTTCATAAGATTATAAATCTATGTTATAATGATAATATAATT 1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ТТАРАРАТАТАСТАТАТТАРТТОГОВТТАСТСОВТТАСССССТТТАТАРТТТАСАРТ 1537
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CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 1030096.8
PRIOR FILING DATE: 2003-01-07
PRIOR PILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR PILING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
SEQ ID NO 568
LENGTH: 5286
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: chemically treated genomic
US-10-517-441-568
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Best Local Similarity
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                                                                                                     GGGATCACTTACTGATCATCCATTAAAACCTTGTTAAAACAAATTCAATGAGATAAAATA 1068
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AGTGTATAGAATTAAATGGGACAGAGGGAGTAATACCTTTATGATAT------AT 1417
                                                                         TTTACTATTTTGAGAAAGTTTTGAAATGTATAGAATTGAGTGGGACATCCATAAAAGGAA 1368
                                                                                                                              CCTCTGAAATGTATACATATGGATTGGACACGGAGACTAAGAAAAATGTATAAAGTAATG
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Pred. No.
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; Sequence 1533, Application US/60655875
; GENERAL INFORMATION:
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TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
FILE REFERENCE: 38-21(53885)
CURRENT APPLICATION NUMBER: US/60/655,875
CURRENT FILING DATE: 2005-02-24
NUMBER OF SEQ ID NOS: 171306
SEQ ID NO 1533
LENGTH: 3999
TYPE: DNA
ORGANISM: Heterodera glycines
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Best Local Similarity
Matches 201; Conserv
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APPLICANT:
APPLICANT:
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NAME/KEY: misc feature
LOCATION: (3964)..(3964)
OTHER INFORMATION: n is a,
-60-655-875-1533
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NAME/KEY: misc feature
LOCATION: (3946)..(3946)
OTHER INFORMATION: n is a,
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TITATGATATATATATTTTTGTTATTTTGATTTCATAAGATTATAAATCTATGTTATAAAT 1465
                                                                             GAGTGGGACATCCATAAAAGGAAAGTGTATAGAATTAAATGGGACAGAGGGAGTAATACC 1405
                                                                                                           GGGGGATTTTTATTTTAAATAATTTCTAAATTTTATCTAATCTTCGATTTTTAGCGGATA
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                                                 AAATATTAAAATGAATGAAGGAGAGATTTTCTAATTTAAGGTAATTAAATTATTTTTT
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Williams, Deryck
Vaudin, Mark
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Lu, Maolong
McCarter, James
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Pred. No. 0.0013;
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; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 24
; LENGTH: 5286
; TYPE; DNA
; ORGANISM: Homo Sapiens
US-10-517-441-24
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CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR APPLICATION NUMBER: DE 1030096.8
PRIOR FILING DATE: 2003-01-07
PRIOR PLICING DATE: 2003-01-07
PRIOR PLICING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 1030096.8
PRIOR PLICING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR FILING DATE: 2002-10-01
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US-10-517-441-24
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Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: FOEKENS, John
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TITLE OF INVENTION: Method and nucleic acids
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
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                                                    ACCTTGTTAAAACAAATTCAATGAGATAAAATATCTTACAATGAAAAGAAGGACAATGTC
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 TCTTTGAAAAAACAAATAGGTACTCCCTCCGTCCCTCTGAAATGTATACATATGGATTGG 1155
                                                                               TTATAACATGTCTCTCGGCTGTCATTATAATAGGGATCACTTACT-GATCATCCATTAAA
                                                                                                                                   GTAAATTTTAAATTAATTGTTATTTTTGTTTCAGAAATTTAAAATAAA 1693
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MAIER, Sabine
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nilarity 44.9%;
Conservative
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                                                                                                                                                                                        Score 65.4; DB 7;
Pred. No. 0.0017;
0; Mismatches 546;
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LENGTH: 8391
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                                                                                                                                                                                                                                                                               TTTCTAAACTTTTTAAAATAAAAAAAAATGCATTATTGTAATAT 1915
                                                                                                                                                                                                                                                                                                                                     ACATCTTTCAAATTTCAACAAACACAGCTTTAACTTTTCTTCAACGGATTGGAATCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTATGTTATAATGATAATATATTTTAAAAATAATACTATATTAATTCTGATTAGTCGAT 1513
                                                                                                                                                                                                                                                                                                                                                                                                                   ATTATTGAGCATGGGAAGTTCACGGGCATCATTGAGCAGCACTAGACTGTTTGAACAATG 1752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAGTAATACCT-TTATGATATATAAATTTTTGTTATTTTGATTTCATAAGATTATAAAT 1453
                                                                                                                                                                                                                                                                                                          TGTATTATATATATATATATATATATATATGTGTATTATATATATATATATATATATATATATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAGTGGGTGGGTGTGAAAAATTTATATATAAAAATTTACTATTTTGAGAAAGTTTTTGAAAA 1334
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                                                                                         OF INDUSTRIAL YEASTS
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US-10-517-441-564
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; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-166179
                                                                                                                                                                                                                                                                           APPLICANT: FOEKENS, John
APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
APPLICANT: MAIER, Sabine
APPLICANT: MARTENS, John
APPLICANT: MODEL, Fabian
APPLICANT: NIMMRICH, Inko
APPLICANT: RUJAN, Tamas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 564, Application US/10517441 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.1%;
Best Local Similarity 45.8%;
Matches 302; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
APPLICANT: MARTENS, John
APPLICANT: MODEL, Fabian
APPLICANT: NIMMRICH, Inko
APPLICANT: RUJAN, Tamas
APPLICANT: SCHMITT, Manfred
APPLICANT: SCHMITT, Manfred
APPLICANT: LOOK, Maxime P.
APPLICANT: HOEFLER, Heinz
APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATTGAGTGGGACATCCATAAAAGGAAAGTGTATAGAATTAAATGGGACAGAGGGAGTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTTTGTAAAACAGCGTTCGGTCAAATGGGAAGTTCATGTGTATTCAATAGTTTTAATAT 1641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAATGATAATATAATTTTAAAAATAATACTATATTAATTCTGATTAGTCGATTACCGCCT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACCTTTATGATATATAAATTTTTGTTATTTTGATTTCATAAGATTATAAATCTATGTTA 1461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTATTAATATATATAGATATAATAGCTTGTATAGTTTAATTGGTTAAAACATTTGTCTC 958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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; Sequence 7091, Application US/60655875
; GENERAL INFORMATION:
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APPLICANT: APPLICANT: APPLICANT:

Guo, Guo, Liang Kovalic, Da Du, Zijing

David

APPLICANT:

Boukharov, Andrey

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

Lu, Maolong McCarter, James Miller, Nancy Williams, Deryck Vaudin, Mark

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CURRENT APPLICATION NUMBER: US/10/517,441
CUBRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/PP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR PILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR PILLNG DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
SEQ ID NO 564
LENGTH: 16579
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                   4454
                                                                                                                                                         4574
                                                                                                                                                                                                                                                                           1476
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                                                                                                                                                                                                                                                                                                                                                                                                                            TCCATAAAAGGAAAGTGTATAGAATTAAATGGGACAGAGGGAGTAATACCTTTATGATAT 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAAGAATTATTGTATAGTAGAGAGAAATTATGTGATTTAGGTGTGAAATTTTATGAATT
                                  AATTAATTGTTATTTTTGTTTCA 1678
                                                                                                                 CGTTCGGTCAAATGGGAAGTTCATGTGTATTCAATAGTTTTAATATAAAAGTAAATTTTA 1655
                                                                                                                                                         ATACTGAGTAATATGAATAAATCAGTTATCTGAAAAGCAAATAATATCTTTGTAAAACAG 1595
                                                                                                                                                                                                                                                                         TITTAAAAATAATACTATATTAATTCTGATTAGTCGATTACCGCCTTTTATAATTTTACA 1535
                                                                                                                                                                                                                                                                                                                   ATAAATTTTTGTTATTTTGATTTCATAAGATTATAAATCTATGTTATAATGATAATATAA 1475
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AATTAGTAAATATAATTTTTTTA 4716
                                                                          TAATAGAGTAGTTTTTGATGTTTTTTTTTTTTTTTTTATTTATATGTTTAGAATATTTAG
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ilarity 45.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 64.6; DB 7;
Pred. No. 0.0027;
0; Mismatches 274;
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; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONT
; TITLE OF INVENTION: IN PLANTS AND COMPOSITI
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/60/655,875
; CURRENT FILING DATE: 2005-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 7091
; ENOTH: 2421
; TYPE: DNA
; ORGANISM: Heterodera glycines
US-60-655-875-7091
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US-10-517-441-290
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APPLICANT:
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APPLICANT: LOCK, Maxime P.
APPLICANT: MARX, Almuth
APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: DE103/010881
PRIOR FILING DATE: 2003-00-1
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10300096.8
                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                             APPLICANT: FOEKENS, APPLICANT: HARBECK
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Local Similarity 49.5%;
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SCHMITT, Armin
SCHMITT, Manfred
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NIMMRICH, Inko
                                                                                                                                                                                                                                                                                                                             HARBECK, Nadia
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-290
Search completed: March 15, Job time: 1980.74 sace
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PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR FILING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
SEQ ID NO 290
LENGTH: 16579
TYPE: DNA
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Local Similarity 45.3%;
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                                                                                 AATTAATTGTTATTTTTGTTTCA 1678
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Pred. No. 0.0053;
0; Mismatches 275;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-352-608-7
US-09-352-608-7
US-09-949-016-12976
US-09-949-016-15853
US-09-949-016-12725
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US-08-911-434A-2
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HYPOTHETICAL: NO
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US-09-949-016-13248	US-09-949-016-11934	US-09-949-016-16110	US-09-949-016-156535	US-09-949-016-146404	US-09-949-016-146136	US-09-949-016-145868	US-09-949-016-37164	US-09-949-016-37150	US-09-949-016-30531	US-09-949-016-146404	US-09-949-016-146403	US-09-949-016-146136	US-09-949-016-146135	US-09-949-016-145868	US-09-949-016-145867	US-09-949-016-37164	US-09-949-016-37163
Sequence 1	Sequence 1	Sequence 1	Sequence 1	Sequence 1	Sequence 1	Sequence 1	Sequence 3	Sequence 3	Sequence :	Sequence 1	Sequence :	Sequence 3					
13248, A	11934, A	16110, A	156535,	146404,	146136,	145868,	37164, A	37150, A	30531, A	146404,	146403,	146136,	146135,	145868,	145867,	37164, A	•

## Sequence 2, Application US/08911434A Patent No. 5959176 GENERAL INFORMATION: APPLICANT: TORIKAI, Satomi APPLICANT: OEDA, Kenji TITLE OF INVENTION: PLANT PROMOTER AND UTILIZATION THEREOF NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS:

ALIGNMENTS

COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,434A
FILING DATE: 12-AUG-1997
CLASSIFICATION: 800
ATTORNEY/AGDWM TO THE PORTY ADDRESSIFICATION: 800 ZIP: 22040 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP STREET: P.O. BOX 747 CITY: FALLS CHURCH STATE: VIRGINIA COUNTRY: UNITED STATES OF AMERICA

ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Raymond C.
REGISTRATION NUMBER: 21,066
REFERENCE/DOCKET NUMBER: 2185.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)205-8050
INFORMATION FOR SEQ ID NO: 2:
SEQUIENCE CHARACTERISTICS:
LENGTH: 2042 base pairs
TYPE: nucleic acid
stranderness: single STRANDEDNESS: single TOPOLOGY: linear DNA (genomic) 2185-0199P

FEATURE: ORGANISM: Daucus carota L.
INDIVIDUAL ISOLATE: Kuroda Kuroda Gosun

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NAME/KEY: LOCATION: promoter 1..2042

Query Match Best Local Similarity 11.8%; 72.8%; Score 241.2; DB 2; Pred. No. 5.4e-42; Length 2042;

Matches

367;

Conservative

0,

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.
APPLICATION NUMBER: US/08/911,434A
FILING DATE: 12-AUG-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Raymond C.
REGISTRATION NUMBER: 21,066
REFERENCE/DOCKET NUMBER: 2185-0199P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: TORIKAI, Satomi
APPLICANT: OEDA, Kenji
TITLE OF INVENTION: PLANT PROMOTER AND UTILIZATION THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1899 ATAATATTTATCAACACCTCAACATTCATGTTAGCGTACTATAAATAGGTGCTCTTGGTG
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                                                                                                                                                                                                                                                   APPLICANT: ISHIGE, Fumiharu
APPLICANT: NISHIGE, Fumiharu
APPLICANT: NISHIGE, Fumiharu
APPLICANT: OEDA, Kenji
TITLE OF INVENTION: Plant Promoter
FILE REFERENCE: 2185-0353P
CURRENT FILLING DATE: 1990-07-13
EARLIER APPLICATION NUMBER: 10-200372 JAPAN
EARLIER APPLICATION NUMBER: 10-200372 JAPAN
SOPTWARE: PILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 20
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 246
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; ORGANISM: Daucus carota
US-09-352-608-2
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US-09-352-608-2
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Best Local S
Matches 222
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Patent No. 6218598
GENERAL INFORMATION:
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Best Local Similarity
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDIVIDUAL ISOLATE: Kuro
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                                           1865
                                                                                NAME/KEY:
LOCATION:
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Similarity 89.5%;
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                   GGAATCCTTTTCTAAACTTTTTAAAATAAAAAAAATGCATTATTGTAATATTTATCAACA 1924
                                                               TCTAGAATATATCTTTTGAAATTTCAACAAACACAGCACTAACTTTTCTTTTAACAGATT
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                                                                                                                                 Score 195.6; DB 3;
Pred. No. 1.7e-32;
0; Mismatches 24;
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- AAAAAATACATTACTATAATATTTATCAACA
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                                                                                                                                                               Length
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RESULT 2 US-08-911-434A-1

Sequence 1, Application US/08911434A Patent No. 5959176

GENERAL INFORMATION:

NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART,
STREET: P.O. BOX 747

STREET: P.O. BOX 7.

VIRGINIA

COUNTRY:

UNITED STATES OF AMERICA

22040

TELEPHONE: (703)205-8000
TELEFAX: (703)205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

TELEPHONE:

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CTCAGCAATAACATTCTAAATATC 2052

TTTAGCAAAACATTCTAAAGGTC 2042

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1790 1781

1721 1730

1670 1603

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Patent No. 6218598
(GENERAL INFORMATION:
APPLICANT: ISHIGE, Fumiharu
APPLICANT: ISHIGE, Fumiharu
APPLICANT: OEDA, Kenji
TITLE OF INVENTION: Plant Promoter
FILE REFERENCE: 2185-0353P
CURRENT APPLICATION NUMBER: US/09/352,608
CURRENT FILING DATE: 1999-07-13
EARLIER APPLICATION UMMBER: 10-200372 JAPAN
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                              US-09-352-608-7/c
; Sequence 7, Application US/09352608
; Patent No. 6218598
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US-09-352-608-6
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CURRENT APPLICATION NUMBER: US/09/352,608
CURRENT FILING DATE: 1999-07-13
EARLIER APPLICATION NUMBER: 10-200372 JAPAN
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 20
SOPTWARE: Patentin Ver: 2.0
SEQ ID NO 6
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
LENGTH: 140
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: ISHIGE, Fumiharu
APPLICANT: NISHIKAWA, Satomi
APPLICANT: OEDA, Kenji
TITLE OF INVENTION: Plant Promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence:primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-949-016-12776
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISSASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12776, Apparent No. 681233
                                                                                                                                                                                                                                                                                                                                           Matches 417;
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Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 187169
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (1)...(187169)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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TCCGTCCCTCTGAAATGTATACATATGGATTGGACACGGAGACTAAGAAAAATGTATAAA 1182
                                                                                                                                                              ATAATAGGGATCACTTACTGATCATCCATTAAAACCTTGTTAAAACAAATTCAATGAGAT 1062
                                                                                                                                                                                                                               CTTTTACAAGAATTTATATTAAACGAAAATCATTTTATAACATGTCTCTCGGCTGTCATT 1002
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                                                       AAAATATCTTACAATGAAAAGAAGGACAATGTCTCTTTGAAAAAAACAAATAGGTACTCCC 1122
                                                                                                                          CATCACATCAATCTTCCAGCACAAACCTTGAGCTTAATCTTTCTACTAATTTTTTAGCAAA 21
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92.6%;
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                                                                                                                                                                                                                                                                                                                                         Score 81.4; DB 4;
Pred. No. 1.4e-07;
0; Mismatches 496;
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; APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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US-09-949-016-15940
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                                                                                        SOFTWARE: FastSEQ for Windows Version SEQ ID NO 15940
                                                                                                                                                                                                                                                                                                Sequence 15940, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
                                                                                                                        NUMBER OF SEQ ID NOS: 207012
 FEATURE: misc_feature LOCATION: (1)...(191569)
                                                TYPE: DNA
ORGANISM: Human
                                                                              ENGTH: 191569
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Best Local Similarity
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Pred. No. 1.4e-07;
0; Mismatches 496;
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GENERAL INFORMATION:

GENERAL INFORMATION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER

FILE REFERENCE: CL001307

CURRENT PELLING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: Fast-SEQ for Windows Version 4.0

1 EEGTH: 205044
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; ORGANISM: Human
; FEATURE:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(205044)
; OTHER INFORMATION: n = A,T
US-09-949-016-15851
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Best Local Similarity
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Patent No. 6812339
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TATATATATTTAAATATAAATATATAAAAATATATTTA 201098
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Pred. No. 1.3e-05;
0; Mismatches 288;
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; ERATURE;
; NAME/KEY: misc_feature
; LOCATION: (1)...(205044)
; OTHER INFORMATION: n = A,T,C or
US-09-949-016-15852
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 15852
LENGTH: 205044
TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: VENTER, J.
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Best Local
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TITLE OF INVENTION: PCLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
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PRIOR TILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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                               TTGTTATTTTTGTTTCAGAAATTAAAATAAATTATTGA 1700
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Pred. No. 1.3e-05;
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US-09-949-016-15853
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR PILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15853, App
Patent No. 6812339
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ORGANISM: Human
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(205044)
OTHER INFORMATION: n = A,T
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Similarity 48.0%;
                      TTGTTATTTTTGTTTCAGAAATTTAAAATTAATTATTGA 1700
                                               TATATATATTTTAAATATAAATATATAAAAATATATTTA 201098
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Pred. No. 1.3e-05;
0; Mismatches 288;
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FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(223471)

OTHER INFORMATION: n = A,T,C

US-09-949-016-12387
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US-09-949-016-12387
; Sequence 12387, Application US/09949016
; Patent No. 6812339
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
WINNERD OF OFF IN NOC. 2077019
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Best Local Similarity 48.0%;
Matches 278; Conservative
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SOFTWARE: FRATSEQ for Windows
SEQ ID NO 12387
LENGTH: 223471
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ORGANISM: Human
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1662 TTGTTATTTTGTTTCAGAAATTTAAAATTAATTGA 1700
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Pred. No. 1.3e-05;
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FABLSEQ for Windows Version 4.4
SEQ ID NO 12724
LENGTH: 223471
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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT APPLICATION NUMBER: E0/241,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR PILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR APPLICATION NUMBER: 60/231,498
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; LOCATION: (1)...(223471)
; OTHER INFORMATION: n = A,T,C
US-09-949-016-12724
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GENERAL INFORMATION:
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ORGANISM: Human
PEATURE:
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                                     ----ATGGGAAGTTCATGTGTATTCAATAGTTTTAATATAAAAGTAAATTTTAAATTAA 1661
                                                                            AATAAATCAGTTATCTGAAAAGCAAATAATATCTTTGTAAAACAGCGTTCGGTCAA----
                                                                                                                                                    TÄTTTTÄÄATATAÄATÄTATAÄAAÄTATATATATTTTÄAATATAÄÄTÄTATÄAAÄÄTÄTÄ 171366
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OF DETECTION AND USES THEREOF
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Best Local Simi:
Matches 278;
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 12725
LENGTH: 223471
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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CURRENT FILING DATE: 2000-04-14
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(223471)
OTHER INFORMATION: n = A,T,C or
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Local Similarity 48.0%;
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                                                                                                     AATAAATCAGTTATCTGAAAAGCAAATAATATCTTTGTAAAACAGCGTTCGGTCAA----
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Pred. No. 1.3e-05;
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US-08-232-463-14/c
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Best Local
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Patent No. 5670367
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
CLONE: pTZgpt-F1s
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBI
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
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         1281
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                                                                                                                                                                                                                                                Similarity
ATAGGTACTCCCTCCGTCCCTCTGAAATGTATACATATGGATTGGACACGGAGACTAAGA 1170
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                                                       TTGTTATTTTTGTTTCAGAAATTTAAAATTAAATTATTGA 1700
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                                                                                                                                                                                                                              3.4%; Score 69.4; DB 1; ilarity 4.6%; Pred. No. 2.4e-05; Conservative 212; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                    (703)683-4109
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; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters
US-09-806-708B-22
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CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.0
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TYPE: DNA
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                  1129 TTKTYKKANININININGMGKDWIRMDATKWSATGTAWWTINHAKRGATMCWYWYWTGTI
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Similarity 13.1%; Pred. No. 2.4e-05;
41; Conservative 392; Mismatches 536
GATNININININININININININISCCTCTRYMTMRWIMKGDGMTVRKKVKWRDTTCTYVDVWAD
                                                                                                                                                                                        ATGTAAACTGATCTAAAGCACATAGAAATTTAGTACAGGTTAAAACTTTTACAAGAATTT
                                                                                                                                                                                                                                                                                                                                                 AAAATTAGAGCTATTAATTAAGTTACTAATAAATAAGAGAGGTTAGTAAACAGAAAGCAG 837
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                                                                           NNNNMWKAYYAHATINIWGCWWNNTDARRTINITTVMRRRWMTNTKTRWYSTTRR---HHYT
                                                                                                                ATATTAAACGAAAATCATTTTATAACATGTCTCTCGGCTGTCATTATAATAGGGATCACT 1017
                                                                                                                                                                                                                                 RNTRTW--WABWKHSWCNNNNNNNNNNNNNNTWCHYTTANABBCYRANNNNAAARMARTC 775
                                                                                                                                                                                                                                                                                                              GAHSKRRTRHHTRTCRRTKYNNNNNNARTVYWYHHAARRWMNAWWTRTNNNNNNNNNNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGYAKSCATNNAMWYATTRWAAYAAAKWARWAGNNMRMYGAAAGNKWGCMAAMATMGBWW 951
                                                                                                                                                       NNYMHAAVTTTHTDWCYKTWMNTWYWDMMTTMBTTTTRNMTTSTNMTNNNNNMWACTNN
                                                                                                                                                                                                                                                                     GTAAAAACAAGAGCTTGCTGCTGTGTGTTTAGTTGTGAGCTCATTTCTTTAAAAGTA 897
                                                                                                                                                                                                                                                                                                                                                                                        ADTAGKMCNNNNNWTTDVRRMAM~~KAKNNNNNNAYWTACYNRAATNNKWATHWMKWTH
                                                                                                                                                                                                                                                                                                                                                                                                                             ACTTGGTCACTGATAAATAGATAATTGTTAGTATAATATAGTAGGATCTACAATGACATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTTGGCCGAATGCTTCTCAAAATGTTTTTTATATGTAAAATAATGCCCCATCCAAGGATA 597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1198 AAGAAAGAGAAAAGTAGGGTAAAGTAGCGGGACCCACCAATATATAATTGATAGATT 1257
                                   1558 САСТТАТСТСАДАЛАССАЛАГЛАТАТСТТТСТАЛАЛАСАСССТТСССТСАЛАТСССАЛАСТТ 1616
                                                                                                         1498 ATTCTGATTAGTCGATTACCGCCTTTTATAATTTTACAATACTGAGTAATATGAATAAAT 1557
                                                                                                                                                                                   1438 TCATAAGATTATAAATCTATGTTATAATGATAATATTAATATTTAAAAATACTATATTA 1497
                                                                                                                                                                                                                                                  1378 AATTAAATGGGACAGAGGGAGTAATACCTTTATGATATATAAATTTTTGTTATTTTGATT 1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1138 TGTATACATATGGATTGGACACGGAGACTAAGAAAATGTATAAAGTAATGTAGAGTAAA 1197
                                                                                                                                                                                                                                                                                                                                                                                                                537 WMMSGBVRMRWAGTMWWRHWNNNNTDTRYYWWWKRWARBTTTVYDSMCNAKSMWRGNNWR 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 YNWCWRMIYMGKIWINNNNNKAWYYRIKIVAWCNNRYYYDTAVWTBKRNYKYCYAYBWY 240
                                                                                                                                                                                                                                                                                                  359 MMRAWNINNINWRBCKTTSWMWWMDHMNTHCTYGNNTWGSAYBMAAM$WWAAGASNBVT 300
                                                                                                                                                                                                                                                                                                                                                                             17 KMWRWTWKYM--WKAACNNNNBKAMYMRVAWMMYSRDTTNTDWMMWTSDWBWHWYTVDYT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                       477 AMKMWWAANNDAGAMDHWTYWMGNNTWMWRRAWKMMNMAWCRRAYCCNNNNNRACVWHKH 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         597 SWYWWYANWMRCRDVTYTRNNTYCKSYAHSYWYWSNNAMWYRRYSARNWSSMARWTTRNN 538
119 CWMNAKAKVRTAMKHWWYYTDRYVSANNTGVRWMMRWCMWWYSMNNRWYYRMGRKYTW 61
                                                                                                                                                    239 YBMYMGKHHWBWWRRABHRSWNWWWVKCRNKYMVSWHYHAMRYBKWABAVGCNNNWKDRM 180
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